

Access DB#

62595

SEARCH REQUEST FORM

Scientific and Technical Information Center

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Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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	Type of Search	Vendors and cost where applicable
Searcher: _____	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Phone #: 4498	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: 3/18/02	Bibliographic _____	Dr.Link _____
Date Completed: 3/18/02	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: 10	Patent Family _____	WWW/Internet _____
Online Time: 10	Other _____	Other (specify) _____

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:28:54 ; Search time 41.88 seconds
(without alignments)

Title: US-09-931-704-2
1036

Sequence: 1 MDLRAGDSWGLACLCIVLM.....KKKMQPPAAAVTLHLGAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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Database :
pir_08:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	124.5	10.2	203	2	JC4645	cardiotrophin-1 -
2	118.5	9.7	203	2	I49153	cardiotrophin-1 -
3	92	7.5	332	2	G86182	hypothetical prote
4	91.5	7.5	201	2	G02312	cardiotrophin-1 -
5	91.5	7.4	182	2	I48378	hairless protein -
6	91	7.5	195	2	JH0680	ciliary neurotroph
7	89.5	7.3	133	2	T38943	conserved guanine
8	89	7.3	733	2	D83588	conserved hypotnet
9	87	7.1	955	2	T00247	zinc finger protei
10	87	7.1	1561	2	T00248	zinc finger protei
11	86.5	7.1	660	2	T34916	transferase - Stre
12	85.5	7.0	560	2	C38604	poly(3-hydroxyalka
13	84.5	6.9	389	2	F72511	probable cystrathio
14	84	6.9	411	2	F75439	probable cell wall
15	84	6.9	559	2	G71327	probable apolipop
16	83	6.8	452	2	A35602	tallness (tll) pro
17	82.5	6.7	542	2	A82965	hypothetical prote
18	82.5	6.7	723	2	B38749	3-phosphatidylinos
19	82	6.7	704	2	T04584	TMY resistance pro
20	80.5	6.6	512	2	G21171	activin receptor S
21	80	6.5	200	1	UNR1CF	ciliary neurotroph
22	80	6.5	460	2	D75493	cell division cycl
23	80	6.5	2261	1	A42548	genome polyprotein
24	79	6.4	812	2	T34180	hypothetical prote
25	79	6.4	1320	2	T30200	protein-tyrosine k
26	78.5	6.4	390	2	T35509	hypothetical prote
27	78	6.4	254	2	T08755	yes-associated pro
28	78	6.4	272	2	T35231	hypothetical prote
29	77.5	6.3	741	2	A85271	hypothetical prote

30	77.5	6.3	7463	2	T36248	clm peptide synthetase
31	77	6.3	342	2	T12891	hypothetical protein
32	77	6.3	344	2	T13457	hypothetical protein
33	77	6.3	520	2	B75332	extracellular solute
34	77	6.3	586	1	WMBEDE	60% early nonstructural
35	77	6.3	587	1	WMBETE	65% early nonstructural
36	77	6.3	733	2	B82965	hypothetical protein
37	76.5	6.2	310	2	A82734	conserved hypothetical
38	76.5	6.2	338	2	T45394	hypothetical protein
39	76.5	6.2	571	2	H70623	putative potassium
40	76.5	6.2	572	2	B72714	putative methionyl
41	76.5	6.2	837	2	T12514	hypothetical protein
42	76.5	6.2	837	2	T12514	putative alpha-man
43	76	6.2	334	2	A55045	putative 3-hydroxy
44	76	6.2	341	2	B83422	putative serine/threo
45	76	6.2	1007	2	E72489	hypothetical protein

ALIGNMENTS

```

RESULT 1
JC4645
cardiotrophin-1 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
C:Accession: J04645
R:Ishikawa, M.; Saito, Y.; Miyamoto, Y.; Kuwahara, K.; Ogawa, E.; Nakagawa, O.; Harada, Y.
Biochem. Biophys. Res. Commun. 219, 377-381, 1996
A:Title: cDNA cloning of rat cardiotrophin-1 (CT-1): Augmented expression of CT-1 gene
A:Reference number: J04645; MUID:96193659
A:Accession: J04645
A:Molecule type: mRNA
A:Residues: 1-203 <ISH>
A:Cross-references: DDBJ:D78591; NID:g1256926; PIDN:BAAL1427 1; PID:g1256927
C:Genetics:
A:Gene: CT-1
C:Keywords: cardiac muscle; cytokine; heart

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[illegible]

RESULT 2

cardiophilin1 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C:Accession: I49153
R:Penhica, D.; King, K.L.; Shaw, K.J.; Luis, E.; Rullmann, J.; Koch, S.; Darbonne, W.
Proc. Natl. Acad. Sci. U.S.A. 92, 1142-1146, 1995
A:Title: Expression cloning of cardiophilin 1, a cytochrome b5 heme b5 induces cardiac myocy
A:Reference number: I49153; MUID:95166785
A:Accession: I49153
A:Status: nucleic acid sequence not shown; translated from GI/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-203 <RES>
A:Cross-references: EMBL:U08366; NID:g710331; PDB:MAC5174; PDB:g710332
C:Genetics:

1025 KDFLSGLDGEGLWSPSSQTSYWHVFRADDAQRTRRFLOLWCPAGACSLLEPGAGC 1079

RESULT 6
ciliary neurotrophic factor - chicken

N:Alternate names: growth-promoting activity protein
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: J06680; PQ0057
R:Jung, D.W.; Parent, A.S.; Cachianes, G.; Esch, F.; Coulombe, J.N.; Nikolics, K.; Eickbush, R.; Parent, A.S.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
A:Title: Cloning, expression during development, and evidence for release of a trophic factor from the chick ciliary ganglion.
A:Reference number: J06680; M01D:92304573
A:Accession: J06680
A:Molecule type: mRNA
A:Residues: 1-195 <LEU>
A:Cross-references: GB:M08082; NID:9211822; PIDN:AAA48784.1; PID:9211823
R:Eckenstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
A:Experimental source: eye
Neuron 4, 623-631, 1990
A:Title: Purification and characterization of a trophic factor for embryonic peripheral neurons.
A:Reference number: PQ0057; M01D:90211978
A:Accession: PQ0057
A:Molecule type: protein
A:Residues: 155-166, X', 168-175 <ECK>
A:Experimental source: sciatic nerves
C:Comment: This is a neurotrophic protein.
C:Superfamily: ciliary neurotrophic factor
C:Keywords: growth factor

Query Match 7.4%; Score 91; DB 2; Length 195;
Best Local Similarity 27.3%; Pred. No. 0.41; 83; Indels 32; Gaps 9;
Matches 51; Conservative 21; Mismatches 32; Gaps 9;
46 LTRYLEHQLRLSLAGTYLNTLGPFPNPPRLGAEPLRATVDEWRSINDKRLTQ 105
Db 23 LARKMSDVTDLDIYVEROG-----LDNSTVAAGVDPAAV--ERWEOGTGRLD 75
OY 106 N---YEAVSHLCLYLRGLNRQA---ATAELRSLA-----HFCSTLQGLLSIAGVMA 152
Db 76 NLAVYRAFRTLLQMLEOEKELGDTDAELGFLAAMLOVSAVYHHEELL-----ELE 130
OY 153 ALGTPPLPPLPGTPPTWPGPAH--SDPLQKMDFWLLEKLOTWLRSAKDDNRLKKMP 211
Db 131 SGCAFAVE---GSEP---PAPRLSLPEOKRLGRLVRLAQMAVRSVRLDRLSKHGP 184
OY 212 PAAAVTL 218
Db 185 SGAAAGL 191

RESULT 7
Probable guanine nucleotide binding protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38943
R:Stein, J.; Church, C.M.; Bartell, B.G.; Rajandream, M.A.; Wood, V.
A:Title: Cloning and characterization of a protein that is related to the EMBL Data Library, May 1997
A:Reference number: Z21819
A:Accession: T38943
A:Molecule type: DNA
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Residues: 1-1313 <SKE>
A:Cross-references: EMBL:Z95396; PIDN:CA08769.1; GSPDB:GN00066; SPDB:SPAC57A7.11
A:Experimental source: strain 972H; cosmid c57A7
C:Genetics: SPDB:SPAC57A7.11
A:Gene position: 1

Query Match 7.3%; Score 89.5; DB 2; Length 1313;

Best Local Similarity 22.8%; Pred. No. 6.2; Indels 69; Gaps 14;
Matches 61; Conservative 32; Mismatches 29; Gaps 14;

OY 15 LCTVLMHLPAY--PALNR-----TGDPGPGPSI-----OKTTLVYLEHQLRS 56
Db 811 LAFLOHLPALHAKSLKSDTDTNSTSDPKPHFVPSYSEKRLINRSESL--AKGLAIS 870
OY 57 LAG-----TYLNTL-----GPP-FNEPDPMPRI GAETLPRAVTL 91
Db 871 LAGSPRASELTLNGENKPAESNLNHLTSKAYGPPAFNELEY-----QSELD 919
OY 92 EYWSLND-----KLRTONYEAYSHLLCYLRL-----NRQAVTAEK LAHCFTS 139
Db 920 PLTSYLFWSKRYTFEPQMPNEDDEPGS--LYNDRLRNRNEKLLYRKLAEVSTN 977
OY 140 -----LQGLLSIAGVMAALGYPLPGTPPTWPGPAHSDFLQKMDFWLKE--- 190
Db 978 GRNQQLMTFNNTIA-----PRKIMHGFEDQL TLDKDI 1013
OY 191 LQTLWLRSAKDDFNRLKKKKOPPAAYT 217
Db 1014 IQYVDMRR-----NRCLNLSKTSASATF 1036

RESULT 8
DB3588
conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PAO)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: DB3588
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrier, P.; Hickey, M.J.; Adams, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.K.; Lacey, S.; Olson, M.V.
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A:Reference number: A82950; M01D:20437337
A:Accession: DB3588
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-733 <STO>
A:Cross-references: GB:AF004483; GB:AE004091; NID:99946313; PID:NA003843.1; GSPDB:GN00066
A:Experimental source: strain PAO1
C:Genetics: PA0454
C:Superfamily: hypothetical protein H11680

Query Match 7.3%; Score 89; DB 2; Length 7
Best Local Similarity 26.6%; Pred. No. 3.3; 66; Indels 68; Gaps 13;
Matches 58; Conservative 26; Mismatches 42; Gaps 13;
OY 28 LNRGDPGPGPSIOKTYDLTYLLE-----HQLSLAGTYLNTLGPFPNPPRLGAEPLRATVDEWRSINDKRLTQNTONEAYSHLLCYLRLNG--ATAELRL 263
Db 230 LNRCHGRGPGPKV-----SKYTLKLYFIADYVERASSSHYPNRLAEAFHSVLRFCQ 263
OY 78 RL-----GAETLPRAVTLDEWRSINDKRLTQNTONEAYSHLLCYLRLNG--ATAELRL 131
Db 284 RLNDQGRKACQALARA-----TRLKQPPD-IA-----DPL LLEDQA 320
OY 132 SLAHF-----CTSLQGLLSIAGVMAALGYPLPGTPPTWPGPAHSDFLQKMDFWLKE--- 190
Db 321 SLBHLRQGSNPMKGLLSL--GALANLTLTDRKLAGA-----SNPDA LADQDSAL 371
OY 188 LKELQTLWLRSAKD--FNRLKKKKOPPAAYTLHGAAG 224
Db 372 LDRSP-----RSIKDAFERLRDOLTP-----TSLFRKH 400

RESULT 9
T00247
zinc finger protein wiz - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999

C:Accession: T00247
 R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Watanabe, A.; Tohyama, M.
 A:Description: Molecular cloning and distinct developmental expression pattern of splice
 A:Reference number: 214130
 A:Accession: T00247
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-955 <MAT>
 A:Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BAA32791.1; PID:d1033757
 A:Experimental source: brain
 C:Genetics:
 A:Gene: w12

Query Match
 Best Local Similarity 7.1%; Score 87; DB 2; Length 955;
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVPAALNRGDDPGPSIQKTYDTRYLEHQLRLAG---TYLNYLGP-----PFNEPPD 73
 Db 615 LPUSPLASRPGKPGAGPT-----QVPR--ELSLSPITSKPSAASYLGPVATKRPLQEDR 667
 QY 74 FNPRLGAETLPRAVDLEWMSLNDKRLTONYEAVSHLCLYRGL---NRQAATAELR 130
 Db 668 FLPAEVKAKTYIOTELPRKA-KTLHEK-----TSHSSTEACCELCGLYFENRKLASHAR 721
 QY 131 RSLAHP 136
 Db 722 AHLROF 727

RESULT 10
 T00248
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
 R:Matsumoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Watanabe, A.; Tohyama, M.
 A:Description: Molecular cloning and distinct developmental expression pattern of splice
 A:Reference number: 214130
 A:Accession: T00248
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1561 <MAT>
 A:Cross-references: EMBL:AB012265; NID:d1227740; PIDN:BAA32790.1; PID:d1033756
 A:Experimental source: brain
 C:Genetics:
 A:Gene: w12

Query Match
 Best Local Similarity 7.1%; Score 87; DB 2; Length 1561;
 Matches 35; Conservative 19; Mismatches 48; Indels 24; Gaps 7;

QY 22 LPVPAALNRGDDPGPSIQKTYDTRYLEHQLRLAG---TYLNYLGP-----PFNEPPD 73
 Db 1221 LPUSPLASRPGKPGAGPT-----QVPR--ELSLSPITSKPSAASYLGPVATKRPLQEDR 1273
 QY 74 FNPRLGAETLPRAVDLEWMSLNDKRLTONYEAVSHLCLYRGL---NRQAATAELR 130
 Db 1274 FLPAEVKAKTYIOTELPRKA-KTLHEK-----TSHSSTEACCELCGLYFENRKLASHAR 1327
 QY 131 RSLAHP 136
 Db 1328 AHLROF 1333

RESULT 11
 T34916
 C:Species: Streptomyces coelicolor

C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 02-Sep-2000
 C:Accession: T34916
 R:Olliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Kaulbach, M.A.
 A:Description: submitted to the EMBL Data Library, January 1998
 A:Reference number: 221558
 A:Accession: T34916
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-640 <COLT>
 A:Cross-references: EMBL:AL021409; PIDN:CAI16181.1; GSPOR:NM 070; SCOEDB:SC3F7.10
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC3F7.10
 C:Superfamily: glycine C-acetyltransferase homology
 F:287-624/Domain: glycine C-acetyltransferase homology <G7A>

Query Match
 Best Local Similarity 7.1%; Score 86.5; DB 2; Length 1;
 Matches 50; Conservative 13; Mismatches 64; Indels 57; Gaps 9;

QY 22 LPVPAALNRGDDPGPSIQKTYDTRYLEHQL---RSLAGTYLWYLPNPPNPPNPP 78
 Db 100 LPVPA-EGTGDPVTEAVAAAROTYORHQLGADLEG-----E 140
 QY 79 LGAETLPRAVDLEWMSLNDKRLTONYEAVSHLCLYRGL---NRQAATAELR 130
 Db 141 LGVDSVLTSTVAEA---TERLGLT-----GAAPDAKATTTTALA---D 179
 QY 139 SLGGLGSIAGYMAALGYPLDPLPGTEPTWPGPAHSDFLQKMDPFI KETQTMWMS 198
 Db 180 ALRGL-----VAAAPGTAPEAAPTGA-APAGRSNAP-----APCAIXGDIHRS 225
 QY 199 ARDF 202
 Db 226 MKDF 229

RESULT 12
 C38604
 C:Species: Pseudomonas oleovorans
 C:Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 08-Sep-2000
 R:Huisman, G.W.; Monink, E.; Meima, R.; Kazemier, B.; Terpstra, P.; Wilholt, B.
 A:Title: Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas oleovorans. Id
 A:Reference number: A38604; MUID:91115830
 A:Accession: C38604
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-560 <HUI>
 A:Cross-references: GB:M58445; NID:g151441; PIDN:AAA25934.1; PID:g151444
 C:Superfamily: poly(3-hydroxyalkanoic acid) synthase phbC
 C:Keywords: nucleotidyltransferase

Query Match
 Best Local Similarity 7.0%; Score 85.5; DB 2; Length 560;
 Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;

QY 77 PRGAETLPRAVDLEWMSLNDKRLTONYEAVSHLCLYRGL---NRQAATAELR 130
 Db 5 PAKGTPLPATSMNVQ-----NAITGLRGR-----DITSTRNVSROS---LRHPLHTA 50
 QY 135 HFCTSLGGLSIAGYMAALGYPLDPLPG-----TEPTWPGPAHSDFLQKMDPFI 190
 Db 51 HHLALGGLGRV-----ILGDTPLQPNRDPRESDPWQGNPFYRKGLOA---YLAQO 101
 QY 191 LOTWLM 196
 Db 102 KOTRLM 107

RESULT 13
 F72511
 Probable cystathionine gamma-synthase APE2068 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999
 C:Accession: F72511
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai
 ara, H.; Takamiya, M.; Mesuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; I
 DNA:Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy
 A:Reference number: A72450; MUID:99310339
 A:Accession: F72511
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <KAW>
 A:Cross-references: DDBJ:AP000063; NID:95105654; PIDN:BA081078.1; PID:95105766
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE2068
 C:Superfamily: O-succinylhomoserine (thiol)-lyase

Query Match	6.98;	Score 84.5;	DB 2;	Length 389;
Best Local Similarity	22.98;	Pred. No. 3.9;		
Matches 47;	Conservative 19;	Mismatches 78;	Indels 61;	Gaps 8

OY	43	TYDLTRYLEHQRLSLAGTYLNTLGPFNPDPENPRPLGAETLPRATVDELVNRS	-----	97
Db	107	TYGSRSLSEMLSSSTGILEVRLAGPWN	-----	150
OY	98	--NDRLRLTQNEAVSHLLCYLRLGNLRQAATLRL	-----	139
Db	151	MANPLRLVRPP	-----	197
OY	140	LQGLLSTAGYWAALGYRLPQPL	-GTEPTWTPGPAHSDFLQKMDENFLKELQWTWMS	198
Db	198	LESLTRYLAGHNDVVGGSLSGRVEEDLEPRLMMKRLTGMQIPDAY	-----	249
OY	199	AKDFNRLKKKMQPPAAATLHLGHA	223	
Db	250	MKTLKARFQSRRAVAVAEWLESH	274	

RESULT 14
F75439
probable cell wall synthesis protein - *Deinococcus radiodurans* (strain R1)
C:Species: *Deinococcus radiodurans*
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
C:Accession: F75439
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.D.;
M.; Shen, M.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Ulterback, T.; Zalewski, C.; M.
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A:Reference number: A75250; MUID:20036896
A:Accession: F75439
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <WHI>
A:Cross-references: GB:AE001958; GB:AE00513; NID:g6458805; PIDN:AAF10649.1; PID:g6458805
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1076
A:Map position: 1

```
Query Match      6 9%; Score 84; DB 2; Length 411;  
Best Local Similarity 24.68% Pred. NO. 4.6;  
Matches    56; Conservative   25; Mismatches   77; Indels   70; Gaps   11  
  
OY       2 DLRAGDSMGLACTGVWHLPAVPALNRRTDPPGCGPSIQKTYTLTRYLEHQRLSLAQTV 61  
:: | | : | : : | || | : | | :: | :
```

Db 212 EVLAADRMALAEELFSEKSLRGPVLLLLSSG -GRGHYAAADVL*-----TLCNTL -GRA 264

QY 62 LNYLGPPEPNEDFENPRLGAEFLPRATVDLEVMRSLNDRKLTONTONEYEASH* -CYLRLGN 124

Db 265 VQVILPAPASROGE-----GTETIGAVY-----H*IFPKRDLR 296

QY 122 ROAAITAEILRSLAHFCTSLQSLSSIGAV---MAALGYLP--QPLPTL* -TPGPAH 175

Db 297 RLKLAASDL-----VWKAAGSLIYAETATGAVPLIYAPILPGE-----EHN 337

QY 176 SDPLQKMDLFWLLKELQTLWM -RSKQDFNRLKKMQPPAAAVTLHIGA 222

Db 338 ADPLERRG-----AGLMARNRHVRVRLRALDPDCHARLSGGA 376

RESULT 15
 G71327
 Probable apolipoprotein N-acyltransferase (cutE) - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 17-Mar-2000
 C:Accession: G71327
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutcliffe, G.G.; Dodson, R.;
 Ison, J.; Kaldan, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Uetrecht, T.;
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference numbers: A71250; MUID:98332770
 A:Accession: G71327
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-559 <COL>
 A:Cross-references: GB:AE001219; GB:AE000520; NID:93322693; P:JDN:AAC65404.1; PID:G3322
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0417
 C:Superfamily: apolipoprotein N-acyltransferase

Query Match	6.9%	Score 84	DB 2	Length 559	
Best Local Similarity	21.6%	Pred. No. 6.8			
Matches	48	Conservative	17	Mismatches 75; Indels 82; Gaps 9	
QY	10	GMLACLC-----	TVLMLPAVALNMTGDPGSPISOKYDI.LTRYV.EHQ	53	
DB	197	GLCYLCLSHYGARYATLGA	RTTL---ALAIYQNMADPMTSTXERKLTTHA	252	
QY	54	LRSLAGTYLNIYGPFPNEDDENPPLGCAETLPR	AVLDLEWBSLNDKLTLELTONYEASHL	113	
DB	253	LRT-----	QTAPLPPTTPYKREKTTLTHASARA	VDVMV---SESLRPYEQRYHV	301
QY	114	L-----	CYLGLNROA-----	ATAEELRRSLAHCTSLQGL	144
DB	302	YNALPAPRPFSAFLRTLCAPLLVGTPLRL	SLGNSSTGCGANAVALLRP-----	DGHV	352
QY	145	GSIAGYMALGYP-----	LPQPLRGTEPTWPGP	173	
DB	353	AOYTGKMOIVPFAELPIWGHMTSVQURLAOM	LAGSESSTWPGP	394	

Search completed: March 18, 2002, 09:32:30
Job time: 216 sec


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QY 97 LNDKRLTQNEYASHLLCYLRLGNROAA-----TAEIIRSLAHCFTSLGGLLSIAGVM 151
DB 84 ---SERLRQDAALALPDLDAVRRQAEINPRAPRLRLSLDEDAARQVRLGAAYEVYL 140
QY 152 AALGY-----PLPQPLPGEPPTWTPGPAHSDFLOKMDPWLKLEIQTWLMRSKADPNRL 205
DB 141 AALGAAGAARGPVEPVYATLTANSTAGTSAKVLGFHVGCLYGEWVSRTEGDLGQL 197

RESULT 2
CTFL_MOUSE
ID CTFL_MOUSE STANDARD: PRT: 203 AA.
AC Q60753;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE CARDIOTROPIN-1 (Ct-1).
GN CTFL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9516785; PubMed=7862649;
RA Pennica D., King K.L., Shaw K.J., Luis E., Rullamas J., Luch S.-M.,
RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,
RA Wood W.I.;
RT "Expression cloning of cardiotrophin 1, a cytokine that induces
RT cardiac myocyte hypertrophy."
RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
CC EXPRESSION IN SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL: U18366; AAC52173.1; -
DR MGD: MGI:105115; Ctfl.
KW Cytokine.
SQ SEQUENCE 203 AA; 21509 MW; 8B3D41A0B3B232F CRC64;

Query Match 9.7%; Score 118.5; DB 1; Length 203;
Best Local Similarity 28.8%; Pred. No. 0.00041;
Matches 51; Conservative 21; Mismatches 88; Indels 17; Gaps 5;

QY 40 IOKTYDLTRYLEHQRLSLAGTYLNYLGPPNEPDPNPRRL---GAETLPRTAVDLEWRS 96
DB 27 IROTHNLARLITKYAEQLLEEVYQGGEPGLPGFSPPRLPLAGLSGPAPSHALPV--- 83
QY 97 LNDKRLTQNEYASHLLCYLRLGNROAA-----TAEIIRSLAHCFTSLGGLLSIAGVM 151
DB 84 ---SERLRQDAALALPDLDAVRRQAEINPRAPRLRLSLDEDAARQVRLGAAYEVYL 140
QY 152 AALGYPL---PQPLPGEPPTWTPGPAHSDFLOKMDPWLKLEIQTWLMRSKADPNRL 205
DB 141 AALGAAGAARGPVEPVYATLTANSTAGTSAKVLGFHVGCLYGEWVSRTEGDLGQL 197

RESULT 3
CTFL_HUMAN
ID CTFL_HUMAN STANDARD: PRT: 201 AA.
AC Q16619;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE CARDIOTROPIN-1 (Ct-1).
GN CTFL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96429882; PubMed=8833032;
RA Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Gery C.L.,
RA Beatty B.G., Wood W.I.;
RT "Human cardiotrophin-1: protein and gene structure, biological and
RT binding activities, and chromosomal localization."
RL Cytokine 8:183-189(1996).
CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
CC PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,
CC THYMUS, TESTIS AND SMALL INTESTINE. LITTLE OR NO EXPRESSION IN
CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD
CC LEUKOCYTES.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL: U43033; AAD12173.1; -
DR EMBL: U43031; AAD12173.1; JOINED.
DR EMBL: U43032; AAD12173.1; JOINED.
DR EMBL: U43030; AAA85229.1; -
DR HSSP: P04002; IWFA.
DR MIM: 600435; -
KW Cytokine.
SQ SEQUENCE 201 AA; 21227 MW; 0235A7B5745F675F CRC64;

Query Match 7.5%; Score 91.5; DB 1; Length 201;
Best Local Similarity 25.9%; Pred. No. 0.14;
Matches 45; Conservative 24; Mismatches 92; Indels 13; Gaps 5;

QY 40 IOKTYDLTRYLEHQRLSLAGTYLNYLGPPNEPDPNPRRLGAETLPRTAVDLEWRS 99
DB 27 IROTHNLARLITKYAEQLLEEVYQGGEPGLPGFSPPRLPVAGI-SAPADSHAGLPVHE 85
QY 100 KLRLTQNEYASHLLCYLRLGNROAA-----TAEIIRSLAHCFTSLGGLLSIAGVM 154
DB 86 RLRL--DAALALPDLDAVRRQAEINPRAPRLRLSLDEDAARQVRLGAAYEVYL 143
QY 155 GYPLPQPLGTEP---TWTPGPAHSDFLOKMDPWLKLEIQTWLMRSKADPNRL 205
DB 144 G--AANRGPRAEPAAATASASATGVPAPKVLGRVCLYGEWVSRTEGDLGQL 195

RESULT 4
HAIR_MOUSE
ID HAIR_MOUSE STANDARD: PRT: 1182 AA.
AC Q61645;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

```

DE HAIRLESS PROTEIN.
 GN HR. Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-Skin;
 RX MEDLINE=94329587; PubMed=8052649;
 RA Cachon-Gonzalez M.B., Fennel S., Coffin J.M., Moran C., Best S.,
 RA Stoye J.P.:
 RT "Structure and expression of the hairless gene of mice."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:7717-7721(1994).
 CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
 CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN, HAIR
 CC FOLLICLES AND INTERFOLLICULAR EPIDERMIS. NO EXPRESSION IN
 CC DERMIS.
 CC -1- DISEASE: HR MUTATION PRODUCES A NUMBER OF PLEIOTROPIC EFFECTS
 CC INCLUDING STRUCTURAL ABNORMALITIES OF EPITHELIAL CELLS IN THE HAIR
 CC FOLLICLES, HAIR LOSS TOWARDS THE END OF THE FIRST HAIR GROWTH
 CC CYCLE, AND THE FAILURE OF SUBSEQUENT HAIR GROWTH CYCLES. OLDER
 CC MICE CARRYING AN HR MUTATION HAVE BEEN REPORTED TO POSSESS ALTERED
 CC RATIOS OF T-CELL-DEPENDENT B-CELL RESPONSES. MICE HOMOZYGOUS FOR
 CC HR MUTATION ARE UNIQUELY SENSITIVE TO UV AND CHEMICALLY INDUCED
 CC SKIN TUMORS.
 CC -----
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 CC -----
 CC DR EMBL: 232675; CAAB3587.1; -
 CC DR MGI: MGI:96223; hr.
 CC KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 KM Metal-binding.
 FT ZN-FING 595 620 C6-TYPE.
 FT DOMAIN 535 540 POLY-GLY.
 SQ SEQUENCE 1182 AA; 127182 MW; EFBBDE62AE81BA40 CRC64;

Query Match 7.5%; Score 91.5; DB 1; Length 1182;
 Best Local Similarity 23.7%; Pred. No. 1.3;
 Matches 70; Conservative 25; Mismatches 99; Indels 101; Gaps 17;

OY 3 LRAGDSWGLACLTIVLHRLAVPALNRTGDRG-----PGP----- 38
 DB 813 LRAGS--GLRKL-----SLPLSPVRLTSPGALLMLQERPRKHGHLRQEHMRQGPV 865
 OY 39 ----STGKTYDLRYLEHOLRLSLAGTY--LNYLGRP-----FNEPDNPRLG 80
 DB 866 LVSGIOKTLRLMGMMEALGLTGGOVOTLTALGPOTNLDTAFWEGFSHPERP----- 921
 OY 81 AETLPRAVDLEWMSLNDK-LRLTON-----YEASHLLCYL-RGLNRQAT 126
 DB 922 --KLDEGSV-LTLHRTLGRKASRVONLASSLPRLPEYCAHCKKLNLAAYLPLGLLHLE 978
 OY 127 AEL-----RRSLAHFCTSLGGLSIGVMAALGYPLPOLPDLPTETPTWPGPAH 175
 DB 979 POLMAATGVASHGHILGTINLCVEGSDLSILVHAEOI-----PPWY--RAQ 1024

OY 176 SDFLQKMD--DFWLKELQTLMR--SAKDFNLKKKMP--PAAVTLHLGAHG 224
 DB 1025 KDFLSGDGGLWSPGSGTSTVWVHFRAQDAQIRRFLOMVCPCAGAGTLEPARG 1079

RESULT 5
 CNTE_CHICK

ID CNTE_CHICK STANDARD; PRT; 195 AA.
 AC 002011;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE CILIARY NEUROROPHIC FACTOR (CNTF) (GROWTH PROMOTING ACTIVITY) (GPA).
 GN CNF OR GPA.
 OS Gallus gallus (chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=92304573; PubMed=1610564;
 RX Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolic R.,
 RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishii R.:
 RT "Cloning, expression during development, and evidence for release of
 RT a trophic factor for ciliary ganglion neurons."
 RL Neuron 8:1045-1053(1992).
 CC -1- FUNCTION: CNTE IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 CC AXOTOMY.
 CC -1- SUBCELLULAR LOCATION: CYTOSOL; MITOCH.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE CNTE FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M80827; AAA48784.1; -
 CC DR PIR: JH0680; JH0680.
 CC DR HSHP: P26441; 1CNT.
 CC DR InterPro: IPR000151; CNTF.
 CC DR Pfam: PF01110; CNTF; 1.
 CC DR ProDom: PD011041; CNTF; 1.
 CC KW Growth factor; Neurone.
 SQ SEQUENCE 195 AA; 21330 MW; FEA076949DB34AC5 CRC64;

Query Match 7.4%; Score 91; DB 1; Length 195;
 Best Local Similarity 27.3%; Pred. No. 0.15;
 Matches 51; Conservative 21; Mismatches 83; Indels 32; Gaps 9;

OY 46 LRRYLEHOLRLSLAGTYLNYLGPENEDPDPRLGAEITLPRAYDLEWV--LRLTNG 105
 DB 23 LARKRSVDTLDDLYVERQG-----LDASISVAADVGVPTAAV--EEMWLVLTORLDD 75
 OY 106 N--YEANSHLLCYRLGNROA--ATAELRRSLA-----HFTSLQGLI--SIACVMA 152
 DB 76 NLAAYRAFTLLAOLMEQRELIGDTDAELGAPALAMLLQYSAVYHLEIL-----ELE 130
 OY 153 ALGYPLPOLPDLPTETPTWPGPAH--SDFLQKMDDEWLKELQTLWMSKNDLNLKKKMP 211
 DB 131 SRAPRAE--GSEP--PAPRLSLFEQKILGLRLBELAQWAVRSVRLPLSKHGPG 184
 OY 212 PAAAVTL 218
 DB 185 SGAALGL 191

RESULT 6
 MIP1_SCHPO STANDARD; PRT; 1313 AA.
 ID MIP1_SCHPO
 AC P87141;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE WD-REPEAT PROTEIN MIP1.
GN MIP1 OR SPAC57A7.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX NCBI_Taxid=4896;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=20115869; PubMed=1064609.
RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.;
RT "Novel WD-repeat protein Mip1 facilitates function of the meiotic
RT regulator Meip1 in fission yeast."
RN Mol. Cell. Biol. 20:1234-1242(2000).
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Skelton J., Churcher C.M., Wood V., Barrell B.G., Rajandream M.A.;
RT Submitted (May-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONJUGATION BY INTERACTING
CC WITH STE11. ESSENTIAL FOR CELL GROWTH.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
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CC -----
DR EMBL; AB032552; BAA84585.1;
DR EMBL; Z95396; CAB08769.1;
DR Interpro: IPR001680; WD40.
DR Pfam: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR SMART: SM00320; WD40; 5.
DR PROSITE: PS00678; WD_REPEATS_1; 1.
DR PROSITE: PS50082; WD_REPEATS_2; 2.
DR PROSITE: PS50082; WD_REPEATS_REGION; 1.
KW Meiosis; WD repeat; Repeat.
FT REPEAT 966 1029 WD 1.
FT REPEAT 1033 1074 WD 2.
FT REPEAT 1087 1126 WD 3.
FT REPEAT 1130 1170 WD 4.
FT REPEAT 1176 1216 WD 5.
FT REPEAT 1219 1259 WD 6.
FT REPEAT 1268 1308 WD 7.
SQ SEQUENCE 1313 AA; 148533 MW; C71B663B0171E7A4 CRC64;

Query Match 7.3%; Score 89.5; DB 1; Length 1313;
Best Local Similarity 22.8%; Pred. No. 2.4;
Matches 61; Conservative 32; Mismatches 69; Indels 105; Gaps 14;
QY 15 LCTVLMHLPAAV--PALNR-----TGDPGPPST-----OKTYDLTRYLEHOLRS 56
DB 811 LAFLLQHPALHAKSLSKDPTNSVTSQPKPHFPVPSYSENKILNRSFSLRSLKGLALS 870
QY 57 LAG-----TYLNYL-----GPP--FNEPDEMPRLGATLPRAYDL 91
DB 871 LAGSDRASSELLNGENKPAESNLHLTSKAVPPAPANELEY-----QSELD 919
QY 92 EWMRLND-----KLRLTQYEAYSLLCYLRGL-----NRQATAEELRSIAHCTS 139
DB 920 PLTGYLDFDWSKKYTERPQNRNEDDEPGS--ICYNQRLMRNRREKLIYTRPLAEVSTN 977
QY 140 -----DGLGLGSIAGVMAALGYPLPQLPPTPTWPPGAHSDFLQKMDFWLKE--- 190
DB 978 GRWNOQLMTFNNTIA-----PRKLMEHQEFQDLITLGDKDI 1013

QY 191 LOTWLRSAKDFNRLKKKMQPPAAVT 217
DB 1014 IQVWDMRR-----NRLNLSFKTSASATV 1036
RESULT 7
HAIR_RAT
ID HAIR_RAT STANDARD; PRT; 1181 AA.
AC P97609;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HAIRLESS PROTEIN.
GN HR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RX MEDLINE=9714510; PubMed=8987811;
RA Thompson C.C.;
RT "Thyroid hormone-responsive genes in developing cerebellum include a
RT novel synaptotagmin and a hairless homolog."
RL J. Neurosci. 16:7832-7840(1996).
CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COU
CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
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CC -----
DR EMBL; U71293; AAC53018.1; ALT_INIT.
DR Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
KW Metal-binding;
FT ZN.FING 594 619 C6-TYPE.
SQ SEQUENCE 1181 AA; 127307 MW; 834B7029CF8E88F0 CRC64;

Query Match 7.1%; Score 87.5; DB 1; Length 1,81;
Best Local Similarity 25.3%; Pred. No. 3.2;
Matches 61; Conservative 21; Mismatches 92; Indels 67; Gaps 12;
QY 30 RTGPGPPSPSTIQKTYDLTRYLEHOLRSIAGTY--LNYLGP-----FNEPP 74
DB 859 RQGQPVLVSGIQKTLRLSLWGMEMALGTLGGQVOTLTLGPPPTSLDSYAFMKGFSPER 918
QY 75 NPPRLGAEETLPRAYDLVWRSINDK-----LRITO-----NEAVSHLIC 115
DB 919 RP-----KIDEGSV--LLHRRPLGDKDESREVENIASLPLPEYCAHQKLNILASVPLDL 971
QY 116 YLNGLNQAAATAEALRS-----LAHFTCSLQGLLSINGVMAALQYPLVYLPPTPTW 169
DB 972 TLHPLPQLMAAYGVNSHSHGLSTKNLCVEVSLILVHAERQL-----PPW 1019
QY 170 TPGPAISDFLOKMD--DFWLKELQTLWLR--SADFNRLKKRMP--PAAAVTLHLGN 223
DB 1020 Y--RAQKDFLSGLDGEGLMSPQSQSTVWHVPRADQAGIRRFQDMVCPAGAGTLEPGAP 1077
QY 224 G 224
DB 1078 G 1078
RESULT 8
PHAC_PSEOL
ID PHAC_PSEOL STANDARD; PRT; 560 AA.

AC P26496;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE POLY(3-HYDROXYALKANOATE) POLYMERASE 2 (EC 2.3.1.-) (PHA POLYMERASE 2)
 DE (PHA SYNTHASE 2) (POLYHYDROXYALKANOIC ACID SYNTHASE 2).
 GN PHAC.
 OS Pseudomonas oleovorans.
 ON Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_Taxid=301;
 RP SEQUENCE FROM N.A.
 RC STRAIN=GP01;
 RX MEDLINE=91115830; PubMed=1969978;
 RA Huisman G.W., Woulik E., Melma R., Kazemier B., Terpstra P.,
 Wiltbold B.;
 RT "Metabolism of poly(3-hydroxyalkanoates) (PHAs) by Pseudomonas
 oleovorans. Identification and sequences of genes and function of the
 encoded proteins in the synthesis and degradation of PHA.";
 RL J. Biol. Chem. 266:2191-2198(1991).
 CC -1- FUNCTION: POLYMERASE ACCUMULATES POLY(3-HYDROXYALKANOATES) AFTER
 GROWTH ON MEDIUM CHAIN LENGTH HYDROCARBONS. LARGE AMOUNTS OF THIS
 POLYESTER ARE SYNTHESIZED WHEN CELLS ARE GROWN UNDER NITROGEN-
 LIMITING CONDITIONS. WHEN NITROGEN IS RESUPPLIED IN THE MEDIUM,
 THE ACCUMULATED PHA IS DEGRADED.
 CC -1- SIMILARITY: BELONGS TO THE PHA/PHB SYNTHASE FAMILY.
 CC -----
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 CC -----
 CC EMBL: M58445; AAA25934.1; -;
 DR PIR: C38604; C38604.
 DR InterPro: IPR000073; Abhydrolase.
 DR Pfam: PF00561; abhydrolase; 1.
 KM PHA biosynthesis; Transferase; Acyltransferase.
 FT ACT_SITE 296 POTENTIAL.
 SQ SEQUENCE 560 AA; 62631 MW; E2CD844FC1616B83 CRC64;

Query Match 7.0%; Score 85.5; DB 1; Length 560;
 Best Local Similarity 30.2%; Pred. No. 1.9;
 Matches 38; Conservative 17; Mismatches 42; Indels 29; Gaps 7;

DB 77 PRGAEPLPATYDLEWMSLNDKLTQNYEAYSHLCLGRLNRQAATLRLSL--A 134
 5 PAKGTPLPTSMNVQ-----NALTLGRG-----DLITLKNVRSOS-----LRHPLHTA 50
 QY 135 HFCSTLGLGSLAGVMAALGYPLPQPLPG---TEPTWPGPANSDFLQKKMDTWLKE 190
 DB 51 HHLALGGLGGRV-----ILGDTPLQPNRDPFRSDPTWSQNFYRGLQA---YLAWQ 101
 QY 191 LQTLWM 196
 DB 102 KQTRLW 107

RESULT 9
 CNTF_PIG STANDARD; PRT; 200 AA.
 ID CNTF_PIG
 AC 002732;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE CILIARY NEUTROTROPHIC FACTOR (CNTF).
 GN CNTF.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
 OX NCBI_Taxid=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98030048; PubMed=9363597;
 RA Weeks R.L., Ramsonder J.J., Gallagher D.S. Jr., Nogueira
 RA Piedrahita J.A.;
 RT "Isolation, characterization and chromosomal localization of the
 porcine ciliary neurotrophic factor (CNF) gene.";
 RL Anim. Genet. 28:354-357(1997).
 CC -1- FUNCTION: CNF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 AXOTOMY (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CNF FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U57644; AAC27342.1; -;
 DR HSSP: P26441; 1CNT.
 DR InterPro: IPR000151; CNTF.
 DR Pfam: PF01110; CNTF; 1.
 DR ProDom: PD011041; CNTF; 1.
 KW Growth factor; Neurone.
 SQ SEQUENCE 200 AA; 22718 MW; 40507C4457ED6531 CRC64;

Query Match 6.9%; Score 84; DB 1; Length 200;
 Best Local Similarity 24.7%; Pred. No. 0.72;
 Matches 47; Conservative 23; Mismatches 88; Indels 32; Gaps 9;

DB 46 LRFYELRHQSLAGTYLNTLSPNEPDRPRLCAELPLPATYDLEWMSLNDKLTQ 105
 DB 23 LARKIRSDTLALMEAVKHOQ--LINE---NINLSDVDPMASTDR--WSEITAEKRLQ 75
 QY 106 NREAYSHLCLGRLNRQAATLRLSLAHFCTS---LQGLSLAGVMAALGYPLPQ-- 160
 DB 76 NLRAYRFFHYMARL-----LEDQREHFPADDDHQAHLHIVLVAAFAVQLEELM 127
 QY 161 -----PLPGTEPTWPGPANSDFLQKKMDTWLKEQTLWMRSKAPNKLKKMQPPA 213
 DB 128 VLEHKVPPSEAGGTPLSVGGGLFEKRLMGKLVQLELSQMTVRSIRDIYVSSHQ----- 183
 QY 214 AAVTLHGAA 223
 DB 184 AGVPAH-GSH 192

RESULT 10
 TLL_DROME STANDARD; PRT; 452 AA.
 ID TLL_DROME
 AC P18102; Q9VA33;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 20-NOV-2001 (Rel. 40, Last annotation update)
 DE TAILLESS PROTEIN.
 GN TLL OR NR2E2 OR CG1378.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Terebrata; Hexapoda; Insecta;
 OC Ephydroidea; Neoptera; Eudopterygota; Diptera; Brachycera; Muscomorpha;
 OX NCBI_Taxid=7227;
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=90304905; PubMed=2364433;

Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ALONG ALA-1022.
 RX MEDLINE=98111413; PubMed=9445480;
 RA Ahmed W., Ul Haque M.F., Brancolini V., Tsou H.C., Ul Haque S.,
 Lam H., Alta V.M., Owen J., Deblagiere M., Frank J.,
 Raeserhaml-Friedman P.B., Leask A., McGrath J.A., Peacocke M.,
 RA Ahmed M., Ott J., Christiano A.M.;
 RT "Alopecia universalis associated with a mutation in the human hairless
 gene";
 RL Science 279:720-724(1998).
 RN [2]
 RP VARIANT APL GLN-620.
 RX MEDLINE=98431781; PubMed=9758627;
 RA Ahmed W., Irvine A.D., Lam H., Buckley C., Bingham E.A.,
 RA Parthey A.A., Ahmed M., McGrath J.A., Christiano A.M.;
 RT "A missense mutation in the zinc-finger domain of the human hairless
 gene underlies congenital atrichia in a family of Irish travellers";
 RL Am. J. Hum. Genet. 63:984-991(1998).
 RN [3]
 RP VARIANT ALUNC ASP-1136, AND ALTERNATIVE SPLICING.
 RX MEDLINE=98409496; PubMed=9736769;
 RA Cichon S., Anker M., Vogt I.R., Rohleder H., Putzstuck M., Hillmer A.,
 RA Farooq S.A., Al-Dhafri K.S., Ahmed M., Haque S., Rletschei M.,
 RA Propping P., Kruse R., Nothen M.M.;
 RT "Cloning, genomic organization, alternative transcripts and mutational
 analysis of the gene responsible for autosomal recessive universal
 congenital alopecia";
 RL Hum. Mol. Genet. 7:1671-1679(1998).
 CC -1- FUNCTION: MAY ACT AS A TRANSCRIPTION FACTOR THAT COULD ACT ON TO
 CC REGULATE ONE OF THE PHASES OF HAIR GROWTH.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN AND SKIN.
 CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ALOPECIA UNIVERSALIS
 CC (ALUNC); A RARE AUTOSOMAL RECESSIVE FORM OF HAIR LOSS. IT IS
 CC CHARACTERIZED BY HAIR FOLLICLES WITHOUT HAIR.
 CC -1- DISEASE: DEFECTS IN HR ARE THE CAUSE OF ATRICHTIA WITH PAPULAR
 CC LESIONS (APL) (ALSO KNOWN AS CONGENITAL ATRICHTIA). THIS AUTOSOMAL
 CC RECESSIVE DISEASE IS CHARACTERIZED BY PAPULAR LESIONS OVER MOST
 CC OF THE BODY AND ALMOST COMPLETE ABSENCE OF HAIR.
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 CC -----
 CC EMBL: AF039196; AAC32258.1; -
 DR EMBL: 602302; -
 DR MIM: 203655; -
 DR MIM: 209500; -
 KW Zinc-finger; DNA-binding; Nuclear protein; Transcription regulation;
 KW Metal-binding; Alternative splicing; Disease mutation.
 FT ZN-FING 600 625
 FT VARIANT 620 620 R -> Q (IN APL);
 FT T -> A (IN ALUNC);
 FT /FTID=VAR_005265;
 FT VARIANT 1022 1022 T -> A (IN ALUNC);
 FT /FTID=VAR_005266;
 FT V -> D (IN ALUNC);
 FT /FTID=VAR_005267;
 FT VARIANT 1136 1136 /FTID=VAR_005267;
 FT SEQUENCE 1189 AA; 127396 MW; 94C8B07AC8AFEE36 CRC64;

Query Match 6.7%; Score 82.5; DB 1; Length 1189;
 Best Local Similarity 23.3%; Pred. No. 9.5;
 Matches 71; Conservative 23; Mismatches 92; Indels 119; Gaps 15;

OY 3 LRAGDSW--GMLACLTVMHLPAPALNRGDPGPGP-----SI 40
 DB 818 LRAGPGLRGLGLPSPVRLPPGALMLDPPGCPFRGHLEOENIKKQVPPVLSGI 877
 OY 41 QRTYDRLRYLEHQLRSIAGTY--LNYLAPP-----FNEEDFNPV----- 77
 DB 878 QRLQGNLMQMTALGALGGVQALSPGPPSSLGSTFEWEGFSPRLRPKSDGGSVLL 937
 OY 78 ---RLGAEPLR-----AYVDEWMSLNDKRLT-----ON AY----- 110
 DB 938 LRRLGDEDESRVENLAASLPPEYCALHKKMLASYPPLGALRPLHQLMNAIVSPH 997
 OY 111 -SH-----LCYLRGLNUNQATFAELRSIAHFCSTLQGLGSLAGVNAALGYPLPPLPCT 165
 DB 998 RGHGTRKNTLC-----VEVADLVSLVHADPPL----- 1024
 OY 166 EPWTTPGPAHSDFLOKMD--DFWLLKELOTWLR--SAKDFNLRKKNP--PAAVTLH 219
 DB 1025 -PAW--HRAQKDFSLGIDGGLWSPGSQSVTWVHVRADQRIRRRLQWVFPVAGAGALE 1081
 OY 220 LGANG 224
 DB 1082 PGAGG 1086
 RESULT 12
 P85B_BOVIN STANDARD; PRT; 724 AA.
 ID P85B_BOVIN
 AC P23726;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PHOSPHATIDYLINOSITOL 3-KINASE REGULATORY BETA SUBUNIT (P85-BETA)
 DE P85-BETA SUBUNIT (PTDINS-3-KINASE P85-BETA).
 GN PIK3R2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91191567; PubMed=1707345;
 RA Otsu M., Hiles I.D., Gout I., Fry M.J., Ruiz-larrea F., Panayotou G.,
 RA Thompson A., Dhand R., Hsuan J., Totty M., Smith A.D., Morgan S.J.,
 RA Courtneidge S.A., Parker P.J., Waterfield M.D.;
 RT "Characterization of two 85 kd proteins that associate with receptor
 RT tyrosine kinases, middle-T/pp60c-src complexes, and p13-kinase";
 RL Cell 65:91-104(1991).
 RN [2]
 RP CIRCULAR DICHOISM AND FLUORESCENCE SPECTROSCOPY.
 RX MEDLINE=93049176; PubMed=1330535;
 RA Panayotou G., Bax B., Gout I., Federwisch M., Wroblewski D., Dhand R.,
 RA Fry M.J., Blundell T.L., Wolmer A., Waterfield M.D.;
 RT "Interaction of the p85 subunit of PI 3-kinase and its minimal SH2
 RT domain with a PDGF receptor phosphorylation site: structural features
 RT and analysis of conformational changes";
 RL EMBO J. 11:4261-4272(1992).
 CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN KINASE
 CC KINASES, THROUGH ITS SH2 DOMAIN, AND ACTS AS AN ADAPTER, MEDIATING
 CC THE ASSOCIATION OF THE P110 CATALYTIC UNIT TO THE PLASMA MEMBRANE.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNITS.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RHO GAP DOMAIN.
 CC -1- SIMILARITY: HIGH, WITH OTHER P85-BETA SUBUNIT, AND A P85 (REGULATORY)
 CC P85-ALPHA SUBUNIT.
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DR EMBL: M61746; AAT9510.1; -
DR HSSP: P23727; 2PNA.
DR InterPro: IPR001720; PI3K_P85.
DR InterPro: IPR000198; RhogAP.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR Pfam: PF006620; RhogAP.1.
DR Pfam: PF00017; SH2.2.
DR Pfam: PF00018; SH3.1.
DR PRINTS: PRO0401; SH2DOMAIN.
DR PRINTS: PRO0678; PI3KINASEP85.
DR SMART: SM00324; RhogAP.1.
DR SMART: SM00252; SH2.2.
DR SMART: SM00326; SH3.1.
DR PROSITE: PSS0001; SH2.2.
DR PROSITE: PSS0002; SH3.1.
DR SH3 domain; SH2 domain.
KW DOMAIN 4 80 SH3.
FT DOMAIN 125 255 RHO-GAP.
FT DOMAIN 326 421 SH2.1.
FT DOMAIN 618 712 SH2.2.
SQ SEQUENCE 724 AA; 81059 MW; 902BA8B6DB087098 CRC64;

Query Match 6.7%; Score 82; DB 1; Length 724;
Best Local Similarity 21.9%; Pred. No. 5.6;

Matches 66; Conservative 25; Mismatches 71; Indels 140; Gaps 16;

QY 6 GDSWGLACLCIVLHLPVPLN-RTGDPGPGPSIQTYDITRYLEHQLSLAGTYLNY 64
DB 42 GVAEGNERQPSVGM-MPGLNERTROKQDFP-----CTIYEEF 77
QY 65 LGP-----PNEPFPNPP-----R 78
DB 78 LGPVALARGPRGRPLPARPRRCPGTLPLDLEQSSPDVAPILVKLEAIER 137
QY 79 LGAETL---PRT-----VDLEWRSINDKRLTONTYEAYSHLCTYLRGLNROAATFAL 129
DB 138 TGLDSYREPPAVRTDMSLSIDVEOW---DAALSDGVKGF-LLALPAPLVTEPAALAA 191
QY 130 RSL-----AHFCTSLQGL---LGSFAG-----VMAALG----- 156
DB 192 HRALEAGAPVGRALERTPLRLHIALTLRLLOHLGRVAGRAPAPGPAVRALGATFGPPL 251
QY 157 -----PLPQPLRGTEPTWT-PGPAHSDFLQKMDFWLKELOQTLWMSAKDFNRKKMKOP 211
DB 252 LRAPPSPSPPGAPDGETPRP---DFPALVLEKTLQEHLE-----EQEVAP 295
QY 212 PA 213
DB 296 PA 297

RESULT 13
ID YM32_MYCTU STANDARD; PRT; 291 AA.
AC 010515: 010516:
DT 01-OCT-1996 (Rel. 34, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOHETICAL 30.7 KDA PROTEIN RV2232/RV2233.
GN RV2232/RV2233 OR MT2292 OR MTCV427.13/MTCV427.14.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV

RX MEDLINE:98295987; PubMed:9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Badoock K., Basham D., Brown D., Brown K., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holtroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.,
RA "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).

RN SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gilm M.L., Holt D., H. Key E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Etmolaeva M.D., Fitzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khoult H., Gill J., Mikula A.,
RA Bishai W.;
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases
CC -1 SIMILARITY: BELONGS TO THE CBBY/CBBZ/GPH/YIEM FAMILY.

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DR EMBL: Z70692; CA94666.1; ALT-TERM.
DR EMBL: Z70692; CA94651.1; ALT-INIT.
DR EMBL: AE007074; AAK46576.1; -
DR TIGR: MT2292;
DR Tuberculist; RV2232;
DR Tuberculist; RV2233;
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 291 AA; 30694 MW; 750F090FB1546E5 CRC64;

Query Match 6.6%; Score 81; DB 1; Length 291;
Best Local Similarity 26.4%; Pred. No. 2.2;
Matches 48; Conservative 15; Mismatches 67; Indels 52; Gaps 11;

QY 23 PAVPALNRIGDPPGPGSIQTYDITRYLEHQLSLAGTY---LNVLGPPFNLYA --- 74
DB 64 PPRAAARRRSPSPSPOL-VIFDLDTLDSARGLVSSFRNALNHGAPVREGDLATHIV 122
QY 75 NPPRLGAEETLP-----RATVLEWRSINDKRLTONTYEAYSHLCTYLR- 118
DB 123 GPPM--HETLRAMGGESEAEIAVAIRADYSARGW-----AMNSLDEGICPLADRT 173
QY 119 -GLNQAAATF-----LRLSLAHF-----CTSLQGLLSIAGVNA-ALGY--PLPQ 160
DB 174 AGVRLAVATSKAEPTRARILRHFGIEQHEFYVJAGASTDSGSKYDVLAHNLQALRPPE 233
QY 161 PL 162
DB 234 RL 235

RESULT 14
ID HUPK_RHOCA STANDARD; PRT; 294 AA.
AC P30797;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPK.
GN HUPK.

OS Rhodobacter capsulatus (Rhodospirillum rubrum capsulatus).
 CC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 CC Rhodobacter.
 ON NCBI_TaxID=1061;
 RX SEQUENCE FROM N.A.
 RA MEDLINE=9177833; PubMed=2007559;
 RT "X. H. W., Wall J.D.;
 RT "Clustering of genes necessary for hydrogen oxidation in Rhodobacter
 RT capsulatus";
 RL J. Bacteriol. 173:2401-2405(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BIO;
 RX MEDLINE=93268090; PubMed=8497190;
 RA Colbeau A., Richard P., Toussaint B., Caballero F.J., Elster C.,
 RA Delphin C., Smith R.L., Chabert J., Vignais P.M.,
 RT "Organization of the genes necessary for hydrogenase expression in
 RT Rhodobacter capsulatus. Sequence analysis and identification of two
 RT hyp regulatory mutants";
 RT Mol. Microbiol. 8:15-29(1993).
 RL -1- SIMILARITY: BELONGS TO THE HUPK FAMILY.
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 CC -----
 DR EMBL: M5089; AA:2924.1; -;
 DR EMBL: Z15089; CA:78803.1; -;
 DR PIR: B38532; B38532.
 DR PIR: S25691; S25691.
 FT CONFLICT 70
 SQ SEQUENCE 294 AA; 30222 MW; 2669E8B70AF35EDA CRC64;
 A -> R (IN REF. 2).
 Query Match 6.6%; Score 80.5; DB 1; Length 294;
 Best Local Similarity 30.5%; Pred. No. 2.5;
 Matches 39; Conservative 3; Mismatches 39; Indels 47; Gaps 6;
 QY 76 PRLGAEITLPRATVDLEWRSNDKRLTQNEYASHLYRGILNQATAE--LRRS 132
 DB 36 PQQVAVELPR-----LFNLGCAAGGHAARLAL-----GLPAEAPARREILRDH 80
 QY 133 LAHFCSTGLGSLGSGVMAALGYPLPQPLPGTEPTTPPGANSDFLQKMDFWLKELO 192
 DB 81 LAKLCLIPKLLGL-----APQPLP-----EHWAEGGA-----ALQ 111
 QY 193 TWLMSRAK 200
 DB 112 HMLMGAK 119
 RESULT 15
 ID BCL_HUMAN STANDARD; PRT; 870 AA.
 AC P56945;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE CRK-ASSOCIATED SUBSTRATE (PI3OCAS) (BREAST CANCER ANTI-ESTROGEN
 DE RESISTANCE 1 PROTEIN).
 GN BCAR1 OR CRKAS OR CAS.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CC NCBI_TaxID=9606;
 CC [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast cancer;

RX MEDLINE=20119429; PubMed=10639512;
 RA Brinkman A., van der Pijl S., Kok E.M., Dorssers L.C.,
 RT "BCAR1, a human homologue of the adapter protein p130CA induces
 RT anti-estrogen resistance in breast cancer cells";
 RL J. Natl. Cancer Inst. 92:112-120(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis.
 RA Otto E., Birbaum S., Verbeek M., Hildebrandt F.,
 RT "Interaction between human Crk-associated substrate (p130CAS) and
 RT nephrin";
 RL submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: DOCKING PROTEIN WHICH PLAYS A CENTRAL COORDINATING ROLE
 CC FOR TYROSINE-KINASE-BASED SIGNALING RELATED TO CELL ADHESION.
 CC IMPLICATED IN INDUCTION OF CELL MIGRATION. OVEREXPRESSION CONTERS
 CC ANTIESTROGEN RESISTANCE ON BREAST CANCER CELLS.
 CC -1- SUBUNIT: FORMS COMPLEXES IN VIVO WITH FOCAL ADHESION KINASE 1,
 CC ADAPTER PROTEIN CRKL AND LYN KINASE. CAN HETERODIMERIZE WITH CASL
 CC (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: FOCAL ADHESIONS. UNPHOSPHORYLATED FORM
 CC LOCALIZES IN THE CYTOPLASM AND CAN MOVE TO THE MEMBRANE UPON
 CC TYROSINE PHOSPHORYLATION (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH AN ABUNDANT EXPRESSION
 CC IN THE TESTIS. LOW LEVEL OF EXPRESSION SEEN IN THE LIVER, THYMUS,
 CC AND PERIPHERAL BLOOD LEUKOCYTES. THE PROTEIN HAS BEEN DETECTED IN
 CC A B-CELL LINE.
 CC -1- DOMAIN: CONTAINS A CENTRAL DOMAIN (SUBSTRATE DOMAIN) CONTAINING
 CC MULTIPLE POTENTIAL SH2-BINDING SITES AND A C-TERMINAL DOMAIN
 CC CONTAINING A DIVERGENT HELIX-LOOP-HELIX (HLH) MOTIF. THE SH2-
 CC BINDING SITES, PUTATIVELY BIND CRK, NCK AND ABL SH2 DOMAINS.
 CC THE HLH MOTIF IS ABSOLUTELY REQUIRED FOR THE INDUCTION OF
 CC PSEUDOPODIAL GROWTH IN YEAST AND MEDIATES HETERODIMERIZATION
 CC WITH CASL (BY SIMILARITY).
 CC -1- DOMAIN: A SERINE-RICH REGION PROMOTES ACTIVATION OF THE SERUM
 CC RESPONSE ELEMENT (SRE).
 CC -1- PTM: FOCAL ADHESION KINASE 1 PHOSPHORYLATES THE PROTEIN AT THE
 CC YDYVHL MOTIF. THE SRC FAMILY KINASES ARE RECRUITED. THE
 CC PHOSPHORYLATED SITES AND CAN PHOSPHORYLATE OTHER TYROSINE
 CC RESIDUES. TYROSINE PHOSPHORYLATION IS TRIGGERED BY INTEGRIN
 CC MEDIATED ADHESION OF CELLS TO THE EXTRACELLULAR MATRIX.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN. NECESSARY FOR THE LOCALISATION
 CC OF THE PROTEIN TO FOCAL ADHESIONS AND INTERACTS WITH ONE PROLINE-
 CC RICH REGION OF FOCAL ADHESION KINASE 1.
 CC -1- SIMILARITY: CONTAINS 1 SH3-BINDING DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE CAS FAMILY.
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 CC -----
 DR EMBL: AJ242987; CAB75875.2; -;
 DR EMBL: AF218451; AAF27527.1; -;
 DR MIM: 602941; -;
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00018; SH3; 1.
 DR SMART: SM00326; SH3; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Phosphorylation; SH3 domain; SH3-binding; Cell adhesion;
 FT DOMAIN 3 65.
 FT DOMAIN 74 87.
 FT DOMAIN 115 416.
 FT DOMAIN 422 614.
 FT DOMAIN 635 643.
 FT DOMAIN 746 796.
 FT DOMAIN 236 236.
 FT CONFLICT 349 349.
 FT CONFLICT 363 363.
 SQ SEQUENCE 870 AA; 93361 MW; D57A9CACAFAAD0 CRC64;
 D -> Y (IN REF. 2).
 A -> G (IN REF. 2).
 I -> T (IN REF. 2).
 SH3-BINDING (POTENTIAL).
 DIVERGENT HELIX-LOOP-HELIX MOTIF.
 SUBSTRATE FOR KINASES (BY SIMILARITY).
 SER-RICH.
 PRO-RICH.
 SH3-BINDING (POTENTIAL).
 DIVERGENT HELIX-LOOP-HELIX MOTIF.

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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:30:24 ; Search time 75.65 seconds
(without alignments)
435.047 Million cell updates/sec

Title: US-09-931-704-2
Perfect score: 1226
Sequence: 1 MDLRAGDSWGMIACTVLM.....KKMKPPAAVTLHGAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP.TREMBL_17:*
2: SP.Archea:*
3: SP.Bacteria:*
4: SP.Fungi:*
5: SP.Human:*
6: SP.Mammal:*
7: SP.Invertebrate:*
8: SP.Plant:*
9: SP.Phage:*
10: SP.Protist:*
11: SP.Virus:*
12: SP.Virus:*
13: SP.Virus:*
14: SP.Virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1226	100.0	225	4 Q9UBD9	Q9UBD9 homo sapien
2	1193	97.3	225	4 Q9QZM3	Q9QZM3 mus musculu
3	130.5	12.3	215	13 Q9PUJ2	Q9PUJ2 plethodon j
4	150.5	12.3	215	13 Q9PUJ1	Q9PUJ1 plethodon j
5	150.5	12.3	215	13 Q9PUJ0	Q9PUJ0 plethodon j
6	148.5	12.1	215	13 Q9PUJ9	Q9PUJ9 plethodon j
7	96.5	7.9	455	11 Q9CWT7	Q9CWT7 mus musculu
8	93	7.6	559	4 Q9G799	Q9G799 homo sapien
9	93	7.6	619	4 Q9G0L2	Q9G0L2 homo sapien
10	93	7.6	619	4 Q9UBU9	Q9UBU9 homo sapien
11	92	7.5	332	10 Q9MAU1	Q9MAU1 arabidopsis
12	92	7.5	423	11 Q9JHE4	Q9JHE4 mus musculu
13	90	7.3	423	11 Q9DBV6	Q9DBV6 mus musculu
14	89.5	7.3	771	2 Q9S3Q9	Q9S3Q9 porphyromon
15	89	7.3	733	2 Q91664	Q91664 pseudomonas
16	88.5	7.2	1429	4 Q9HAV8	Q9HAV8 homo sapien
17	87	7.1	955	11 Q98287	Q98287 mus musculu
18	87	7.1	1561	11 Q98286	Q98286 mus musculu
19	86.5	7.1	640	2 Q54153	Q54153 streptomyce

20	85.5	7.0	1154	11 Q921R2	Q921R2 mus musculu
21	85	6.9	727	11 Q98841	Q98841 mus musculu
22	84.5	6.9	294	11 Q9CP21	Q9CP21 mus musculu
23	84.5	6.9	389	11 Q91A71	Q91A71 aeryopyrum p
24	84	6.9	294	4 Q9NXX5	Q9NXX5 homo sapien
25	84	6.9	411	2 Q9RVP3	Q9RVP3 delinococcus
26	84	6.9	559	2 Q83432	Q83432 treponema p
27	84	6.9	875	4 Q9P210	Q9P210 homo sapien
28	83.5	6.8	310	4 Q9S159	Q9S159 homo sapien
29	83.5	6.8	5990	2 Q9RLP6	Q9RLP6 mycobacteri
30	83	6.8	222	2 Q9LS84	Q9LS84 streptococc
31	83	6.8	625	4 Q16205	Q16205 homo sapien
32	83	6.8	1620	4 Q9Y4K6	Q9Y4K6 homo sapien
33	82.5	6.7	310	4 Q9UID0	Q9UID0 homo sapien
34	82.5	6.7	542	2 Q9HTD5	Q9HTD5 pseudomonas
35	82.5	6.7	1189	4 Q9NPE1	Q9NPE1 homo sapien
36	82	6.7	283	2 Q92B87	Q92B87 pseudomonas
37	82	6.7	1179	10 Q65507	Q65507 arabidopsis
38	82	6.7	2376	10 Q9F1N7	Q9F1N7 arabidopsis
39	81.5	6.6	396	2 Q9AF00	Q9AF00 frankia sp.
40	81	6.6	328	12 Q9E125	Q9E125 human immun
41	81	6.6	328	12 Q9E122	Q9E122 human immun
42	81	6.6	618	11 Q98984	Q98984 rattus norv
43	80.5	6.6	924	2 Q9X582	Q9X582 rhodothermu
44	80.5	6.6	305	4 Q9H7R6	Q9H7R6 homo sapien
45	80.5	6.6	385	2 Q9AD13	Q9AD13 streptomyce

ALIGNMENTS

RESULT 1
Q9UBD9 PRELIMINARY: PRT; 225 AA.

AC Q9UBD9; 01-MAY-2000 (TREMBLrel. 13, Created)
DT DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE NEUROTHROPHIN-1/B-CELL STIMULATING FACTOR-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homn.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99432254; Pubmed=10500198;
RA Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,
RA Simonet W.S., Boone T., Chang M.-S.;
RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cy... line of the
RT IL-6 family.";
RT Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99382254; Pubmed=10448081;
RA Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J.,
RA Ruben S., Alderson R.F.;
RT "Computational EST database analysis identifies a novel member of the
RT neuropeptide cytokine family.";
RL Biochem. Biophys. Res. Commun. 262:132-138(1999).
DR EMBL: AF176912; AAF00992.1; -;
DR EMBL: AF172854; AAD54284.1; -;
DR EMBL: AF176911; AAF00991.1; -;
SQ SEQUENCE 225 AA; 25176 MW; E2DDAB6280833B55 CRC64;

Query Match 100.0%; Score 1226; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 8.5e-109; Indel 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 0;

QY 1 MDLRAGDSWGMIACTVLMHPAIPALNRGDPGPGSIQKTYDLYRLQLSLAGT 60
DB 1 MDLRAGDSWGMIACTVLMHPAIPALNRGDPGPGSIQKTYDLYRLQLSLAGT 60

QY 61 YLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLCYRLG 120
 DB 61 YLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLCYRLG 120
 QY 121 NROAAATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWTGPAHSDFIQ 180
 DB 121 NROAAATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWTGPAHSDFIQ 180
 QY 181 KMDDFWLKELQTWLMSAKDFNRLKKKQPPAAATVTLHGAGF 225
 DB 181 KMDDFWLKELQTWLMSAKDFNRLKKKQPPAAATVTLHGAGF 225

RESULT 2
 ID Q9QZM3 PRELIMINARY: PRT: 225 AA.
 AC Q9QZM3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE NEUROTROPIN-1/B-CELL STIMULATING FACTOR-3.
 GN BSF3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99432254; PubMed=10500198;
 RA Senaldi G., Varum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
 RA Guo J., Elliott G., McIninch J., Shaklee C.L., Freeman D., Mann F.,
 RA Simonet W.S., Boone T., Chang M.-S.;
 RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the
 RT IL-6 family."
 RL Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463 (1999).
 DR EMBL: AF176913; AAF00993.1;
 DR MGI: MGI:1930088; Bsf3.
 SQ SEQUENCE 225 AA; 25261 MW; 68B1FEAAB7F1A950 CRC64;

Query Match 97.3%; Score 1193; DB 11; Length 225;
 Best Local Similarity 96.9%; Pred. No. 1.2e-105;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 1 MDLRAGDSMGWLACTCYLWHLPAVPAALNRTGDPGPGPSIQKTYDRLRYLHQLRSAGT 60
 DB 1 MDLRAGDSMGWLACTCYLWHLPAVPAALNRTGDPGPGPSIQKTYDRLRYLHQLRSAGT 60
 QY 61 YLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLCYRLG 120
 DB 61 YLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLCYRLG 120
 QY 121 NROAAATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWTGPAHSDFIQ 180
 DB 121 NROAAATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWTGPAHSDFIQ 180
 QY 181 KMDDFWLKELQTWLMSAKDFNRLKKKQPPAAATVTLHGAGF 225
 DB 181 KMDDFWLKELQTWLMSAKDFNRLKKKQPPAAATVTLHGAGF 225

RESULT 3
 ID Q9PUJ2 PRELIMINARY: PRT: 215 AA.
 AC Q9PUJ2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE RECEPTIVITY FACTOR ISOFORM 1 PRECURSOR.
 GN PRF.
 OS Plethodon jordanii (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodonti
 OC Plethodon.
 OX NCBI_Taxid=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in
 RT salamander."
 RL Science 285:1907-1909 (1999).
 DR EMBL: AF181480; AAF01025.1;
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 215 AA; 24138 MW; B1906BB66335738 CRC64;

Query Match 12.3%; Score 150.5; DB 13; Length 215;
 Best Local Similarity 26.2%; Pred. No. 1.5e-06;
 Matches 42; Conservative 31; Mismatches 80; Indels 7; Gaps 3;
 QY 56 SLAGTYLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLC 115
 DB 56 SLAGTYLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLC 115
 QY 116 YLR-GLNQ----AATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWT 170
 DB 116 YLR-GLNQ----AATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWT 170
 QY 171 PGPAHSDFIQKMDDFWLKELQTWLMSAKDFNRLKKKQ 210
 DB 171 PGPAHSDFIQKMDDFWLKELQTWLMSAKDFNRLKKKQ 210
 QY 173 PFEGSAVFRKKRLGKGVCKREKRVLLTKRDFELAKKQ 212
 DB 173 PFEGSAVFRKKRLGKGVCKREKRVLLTKRDFELAKKQ 212

RESULT 4
 ID Q9PUJ1 PRELIMINARY: PRT: 215 AA.
 AC Q9PUJ1;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DE 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE RECEPTIVITY FACTOR ISOFORM 2 PRECURSOR.
 GN PRF.
 OS Plethodon jordanii (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodonti; Pleth.
 OX NCBI_Taxid=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99420364; PubMed=10489368;
 RA Rollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial
 RT salamander."
 RL Science 285:1907-1909 (1999).
 DR EMBL: AF181481; AAF01026.1;
 KW Signal.
 FT SIGNAL
 SQ SEQUENCE 215 AA; 24080 MW; B341BBB7B4E28438 CRC64;

Query Match 12.3%; Score 150.5; DB 13; Length 215;
 Best Local Similarity 26.2%; Pred. No. 1.5e-06;
 Matches 42; Conservative 31; Mismatches 80; Indels 7; Gaps 3;
 QY 56 SLAGTYLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLC 115
 DB 56 SLAGTYLNTLGPPFNPDPNPRLGAETLPRAVDLEWRSINDKRLTQNEAYSHLLC 115
 QY 116 YLR-GLNQ----AATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWT 170
 DB 116 YLR-GLNQ----AATLRLSLAHFCTSLQGLGSIAGVMAALGYPLPPLPCTEPTWT 170
 QY 171 PGPAHSDFIQKMDDFWLKELQTWLMSAKDFNRLKKKQ 210
 DB 171 PGPAHSDFIQKMDDFWLKELQTWLMSAKDFNRLKKKQ 210

DB 173 PEGSAYFRKRLGGVCKEYKERVLLTKRDEFLAKTYQ 212

RESULT 5

Q9PU0 PRELIMINARY; PRT; 215 AA.

AC Q9PU0; 01-MAY-2000 (Tremblrel, 13, Created)

DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)

DE 01-MAY-2000 (Tremblrel, 13, Last annotation update)

DE RECEPTIVITY FACTOR ISOFORM 3 PRECURSOR.

GN Pletodon jordani (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidae; Pletodontidae;

OC Pletodon.

OC NCBI_TaxID=8336;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=99420364; PubMed=10489368;

RA Rollman S.M., Houck L.D., Feldhoff R.C.;

RT "Proteinaceous pheromone affecting female receptivity in a terrestrial salamander";

RL Science 285:1907-1909(1999).

DR EMBL: AF181482; AAF01027.1; -.

KW Signal.

FT SIGNAL.

SQ SEQUENCE 215 AA; 24024 MW; 6EB6E64AD9A1343 CRC64;

Query Match 12.3%; Score 150.5; DB 13; Length 215;

Best Local Similarity 27.1%; Pred. No. 1.5e-06;

Matches 45; Conservative 34; Mismatches 72; Indels 15; Gaps 4;

QY 56 SLATYLVNLTGPPNPPRGAETLPRAVDLEWRSINDKRLTONYEAVSHLLC 115

DB 55 SLPTLYLSFGAPLSDPDYOLPHIKVNLPTAANDYOTFIRQDETRKNNLYSAIVE 114

QY 116 YLR-----GLN--KQATAEIIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPTE 166

DB 115 FLKAMTEQEDLNPAELSLKAFEEAMANSNT---LISKISDINTQMGMSVITTEP--K 168

QY 167 PTWTPRAHSDFLQKMDFFLKLQWIMRSKDFNRKKMKMP 212

DB 169 PLVVPKGSAYFSKRLGGVCKEYKERVLLTKRDEFLAKTYQ 214

RESULT 6

Q9PU0 PRELIMINARY; PRT; 215 AA.

AC Q9PU0; 01-MAY-2000 (Tremblrel, 13, Created)

DT 01-MAY-2000 (Tremblrel, 13, Last sequence update)

DE 01-MAY-2000 (Tremblrel, 13, Last annotation update)

DE RECEPTIVITY FACTOR ISOFORM 4 PRECURSOR.

GN Pletodon jordani (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidae; Pletodontidae;

OC Pletodon.

OC NCBI_TaxID=8336;

OX [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=99420364; PubMed=10489368;

RA Rollman S.M., Houck L.D., Feldhoff R.C.;

RT "Proteinaceous pheromone affecting female receptivity in a terrestrial salamander";

RL Science 285:1907-1909(1999).

DR EMBL: AF181483; AAF01028.1; -.

KW Signal.

FT SIGNAL.

SQ SEQUENCE 215 AA; 24054 MW; AAA412135FPA4E7F CRC64;

Query Match 12.1%; Score 148.5; DB 13; Length 215;

Best Local Similarity 25.9%; Pred. No. 2.3e-06;

Matches 42; Conservative 33; Mismatches 80; Indels 7; Gaps 3;

QY 56 SLATYLVNLTGPPNPPRGAETLPRAVDLEWRSINDKRLTONYEAVSHLLC 115

DB 55 SLPTLYLSFGAPLSDPDYOLPHIKVNLPTAANDYOTFIRQDETRKNNLYSAIVE 114

QY 116 YLR--GLNRQ---AATAEIRSLAHFCTSLQGLGSIAGVMAALGYPLPOLPTE 170

DB 115 FLKAMTEQEDLNPAELSLKAFEEAMANSNTLISKISDINTQMGMSVITTEP--KPLVV 172

QY 171 PGPRAHSDFLQKMDFFLKLQWIMRSKDFNRKKMKMP 212

DB 173 PKGSAYFSKRLGGVCKEYKERVLLTKRDEFLAKTYQ 214

RESULT 7

Q9CW7 PRELIMINARY; PRT; 455 AA.

AC Q9CW7; 01-JUN-2001 (Tremblrel, 17, Created)

DT 01-JUN-2001 (Tremblrel, 17, Last sequence update)

DE 01-JUN-2001 (Tremblrel, 17, Last annotation update)

DE 2410003H12RIK PROTEIN.

GN 2410003H12RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

OX [1]

RN SEQUENCE FROM N.A.

RP STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;

RC MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Aizawa T., Hara A., Fukunishi Y., Konno H., Adachi S., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,

RA Saito T., Okazaki H., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Okenobush J.,

RA Schriml L.M., Stabli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Galibardi M.,

RA Gustincich S., Hill D., Hornann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,

RA Wyszynski B., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,

RA Hayashizaki Y.,

RA "Functional annotation of a full-length mouse cDNA collection";

RL Nature 409:685-690(2001).

RT EMBL: AK010358; BAB26878.1; -.

DR MGI:1919221; 2410003H12RIK.

SQ SEQUENCE 455 AA; 51481 MW; 201886B814EB9CFE CRC64;

Query Match 7.9%; Score 96.5; DB 11; Length 455;

Best Local Similarity 22.4%; Pred. No. 0.5;

Matches 59; Conservative 24; Mismatches 89; Indels 91; Gaps 12;

QY 7 DSCGMALACLTVM--HLPAYPALNRGDDG-----GSPSIOKTYDITRLEHQLNS 56

DB 29 DAFVYOSCFMODLFAHPEVLFHRTYNPGRKVLVYFLVDGPNVQEGPLARV----- 82

QY 57 LAGTYLVNLTGPPNPPRGAETLPRAVDLEWRSINDKRLTONYEAVSHLLC 104

DB 83 -----YFALPTNEDARGLAQMEQVFKKFP-----AMERVNTTL--- 116

OY 105 QNENAVSHLLCYLGLNROQATAEIARSLAHFCTSLQGLLSIAGVMAALGYPLPOP--- 161
 Db 117 -----VDHFL-LPFTLMEFTAEVLLSAFHICKFLOGKRYQL-----PLEQPVQR 162
 OY 162 -----LPGTEPTWTPGPAH-----SDFLQKDDFWLKEIQLTWM---WRSKADF 202
 Db 163 LLSSLSLOSTWCSATAGMLRKLTYLLNNCIDSSRLPELHSHWLLND-RTWLAHRRSRAQS 221
 OY 203 NRLKKMQPPAAAVTLHGAHGF 225
 Db 222 SRYFQSLIMAHILISQFFGTTF 244

RESULT 8
 ID 099799 PRELIMINARY; PRT; 559 AA.
 AC 099799;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DE TIP ASSOCIATING PROTEIN.
 GN TAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97318898; PubMed-9175835;
 RA Yoon D.W., Lee H., Seol W., Demaria M., Rosenzweig M., Jung J.U.;
 RT "Tap: a novel cellular protein that interacts with tip of herpesvirus
 RL salivari and induces lymphocyte aggregation.";
 DR EMBL: U60073; AAB8111.1; -
 DR InterPro: IPR001611; LRR.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00446; LRRcap. 1.
 SQ SEQUENCE 559 AA; 63301 MW; 250C136C62042C0C CRC64;

Query Match 7.6%; Score 93; DB 4; Length 559;
 Best Local Similarity 24.7%; Pred. No. 1.4;
 Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

OY 5 AADSMGML-----ACLCYVLMHLPVPAVPAALNRTGDP-GPEPSIOKTYDIT--RYLEHQL 54
 Db 340 SDDRQGLDAYHDGACCSLSIFIPQNPARRSLAEYFKDSRNKYLKDPFLRLKHTR 399
 OY 55 RSLAGTYLNYLGPFPNPPDPNP--PRIGAETLPRAVVDL-----EYWRSLNDKLR-LTON 106
 Db 400 LNVV-AFLNEL--PKQHDVNSFYVDISQSTILCFSVNGVKEVDGKSRSLSRAFTRT 456
 OY 107 Y---EAYSHLLCYLRG--LNROQATAEIARSLAHFCTSLQGLLSIAGVMAALGYPLPOP 161
 Db 457 FIAVPASNSGICIVNDELFRNASSEIQRAPA-----MPAP 493
 OY 162 LPGEPTWTPGPAHSDFLQK-----MDDFWLKEIQLTWM---WRSKADFNRKKMQPP 212
 Db 494 TPSSSPVPTLSPQEQMLQAFSTQSGMNLWESQKCLQDNNMDYTRSAQAFTHLKAGEIP 553
 OY 213 AAA 215
 Db 554 EVA 556

RESULT 9
 ID 090012 PRELIMINARY; PRT; 619 AA.
 AC 090012;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE TIP-ASSOCIATED PROTEIN TAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zolotukhin A.S., Tan W., Bear J., Tabernero C., Feldner B.K.;
 RL Submitted (FE8-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF126246; AAD20016.1; -
 DR InterPro: IPR001611; LRR.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00446; LRRcap. 1.
 SQ SEQUENCE 619 AA; 70195 MW; 092D38037610BF3A CRC64;

Query Match 7.6%; Score 93; DB 4; Length 619;
 Best Local Similarity 24.7%; Pred. No. 1.6;
 Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

OY 5 AGDSMGML-----ACLCYVLMHLPVPAVPAALNRTGDP-GPEPSIOKTYDIT--RYLEHQL 54
 Db 400 SDDRQGLDAYHDGACCSLSIFIPQNPARRSLAEYFKDSRNKYLKDPFLRLKHTR 459
 OY 55 RSLAGTYLNYLGPFPNPPDPNP--PRIGAETLPRAVVDL-----EYWRSLNDKLR-LTON 106
 Db 460 LNVV-AFLNEL--PKQHDVNSFYVDISQSTILCFSVNGVKEVDGKSRSLSRAFTRT 516
 OY 107 Y---EAYSHLLCYLRG--LNROQATAEIARSLAHFCTSLQGLLSIAGVMAALGYPLPOP 161
 Db 517 FIAVPASNSGICIVNDELFRNASSEIQRAPA-----MPAP 553
 OY 162 LPGEPTWTPGPAHSDFLQK-----MDDFWLKEIQLTWM---WRSKADFNRKKMQPP 212
 Db 554 TPSSSPVPTLSPQEQMLQAFSTQSGMNLWESQKCLQDNNMDYTRSAQAFTHLKAGEIP 613
 OY 213 AAA 215
 Db 614 EVA 616

RESULT 10
 ID 090B09 PRELIMINARY; PRT; 619 AA.
 AC 090B09;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE TIP ASSOCIATING PROTEIN (NUCLEAR RNA EXPORT FACTOR 1).
 GN TAP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-99219874; PubMed-10202159;
 RA Braun I.C., Rohrbach E., Izaurralde E.;
 RT "Tap binds to the retroviral constitutive Transport Element through a
 RT novel RNA-binding motif which also mediates CTE-dependent RNA export
 RL from the nucleus.";
 RL EMBO J. 18:1966-1973(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Kang Y., Bogerd H., Izaurralde E., Cullen B.R.;
 RT "A novel RNA binding domain in human Tap protein is necessary but not
 RT sufficient for the nuclear export of mRNA containing Mason-Pfizer
 RT monkey virus constitutive transport element.";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=CHORIOCARINOMA;

RA STRAUSBERG R.
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ132712; CAI10753.1;
 DR EMBL: AF112880; AAD39102.1;
 DR EMBL: BC004504; AAH04504.1;
 DR InterPro: IPR001611; LRR.
 DR InterPro: IPR003603; LRRCD.
 DR PRINTS: PR00019; LEURICHRPT.
 DR SMART: SM00446; LRRcap.1.
 SQ SEQUENCE 619 AA; 70182 MW; 338872AADA789FBF CRC64;

Query Match 7.6%; Score 93; DB 4; Length 619;
 Best Local Similarity 24.7%; Pred. No. 1.6; Mismatches 93; Indels 58; Gaps 13;
 Matches 60; Conservative 32; Mismatches 93; Indels 58; Gaps 13;

QY 5 AGDSMGML-----ACLTCTVLMHLPAVPALNRTGDP--GPGPSIQKTYLDT---RYLEHQL 54
 DB 400 SGRDGLDAHDAGACCSLSIFIPONPARSSIAEYFKDSNNVKLLKDPFLRLKHTR 459
 QY 55 RSLAGTYLNTGPPNEPDENP--PRGAEPLPRATVDL-----EYWSLNDKLR-LQN 106
 DB 460 LNVV-AFLNEL--PKQHDVNSFVVDISAQSTLLCFSGVGVKEDGKSRDLSRAFTRT 516
 QY 107 Y---EAYSHLCYLRG--LNRQAAATLRLSLAHCTSLQGLGSLAGVMAALGYPLDP 161
 DB 517 FIAPVANSGLCIYNDLFLVKNASSEIQRAPA-----MAP 553
 QY 162 LPGTEPTWTPGPAHSDFLOK-----MDDFMLLKELOTWLV--RSANDENLKKKKMP 212
 DB 554 TPSSSPVPTLSPQEOEMLQAFSTGSGMNLWMSQKCLQDNNDYTRSAQAFHLKAKEIP 613
 QY 213 AAA 215
 DB 614 EVA 616

RESULT 11
 ID 09MAU1 PRELIMINARY; PRT; 332 AA.
 AC 09MAU1;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE F13M7.8 PROTEIN.
 GN F13M7.8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 CC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Kwan A., Liu, S.,
 RA Li J., Kremenetskaia I., Luros J., Araujo R., Au M., Bredel V.,
 RA Buehler E., Conway A., Dewar K., Feng J., Kim C., Kurtz D., Li Y.,
 RA Palm C., Shim P., Sun H., Davis R., Ecker J., Federspiel N.,
 RA Theologis A.;
 RT "The sequence of BAC F13M7 from Arabidopsis thaliana chromosome 1.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RP [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Theologis A.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 RP [4]
 RP SEQUENCE FROM N.A.

RC STRAIN=CV. COLUMBIA;
 RA Theologis;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases
 DR EMBL: AC004809; AAF40444.1;
 DR InterPro: IPR002965; P-rich_extensn.
 DR PRINTS: PR01217; PRICHEXTENS.
 SQ SEQUENCE 332 AA; 36793 MW; 18E8687141A070F4 CRC64;

Query Match 7.5%; Score 92; DB 10; Length 377;
 Best Local Similarity 26.4%; Pred. No. 0.92; Mismatches 72; Indels 66; Gaps 13;
 Matches 58; Conservative 24; Mismatches 72; Indels 66; Gaps 13;

QY 23 PAVPALNRTGDPGPPPSIQKTYDRLRYLEHQLSLAGTYLNT----- 64
 DB 113 PSYVAGNLGGY-PPSP--TYDPPGYEQRQWESLQGFIRERNPQIRPLPLGLGSPYG 169
 QY 65 LGPPNEPDENPRLGAEPLPRATVDLEWWSLNDKLRITQWVAYSHLCYLRGINQA 124
 DB 170 LGPIASPOFLQPRVAP--PISILD-----ISRNNKAR-----SKDGLAVVRG--KKV 215
 QY 125 ATAEIRSL-----AHFCTSLQGLGSLAGVMAALGYPLDP 170
 DB 216 RTEGSSSLYSIGRSWLNKAHV-----GIQPORSGIMK-----PLKPLUPVHUTTSVP 266
 QY 171 PGPAHSDFLOKMDDFMLLKELOTWLMRSKADENFLKKKK 210
 DB 267 DDPDEBSADEKDEBAYAKQL-----SEKDL--LKRRIE 298

RESULT 12
 ID 09JHE4 PRELIMINARY; PRT; 423 AA.
 AC 09JHE4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE CEREBROSIDE SULFOTRANSFERASE.
 GN CST.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20193614; PubMed=10727929;
 RA Hirahara Y., Tsuda M., Wada Y., Honke K.;
 RT "CDNA cloning, genomic cloning, and tissue-specific regulation of
 RT mouse cerebroside sulfotransferase.";
 RL Eur. J. Biochem. 267:1909-1917(2000).
 DR EMBL: AB032940; BAA93009.1;
 DR EMBL: AB032939; BAA93008.1;
 DR MGD; MGI:1858277; Cst.
 KW Transferrase.
 SQ SEQUENCE 423 AA; 48984 MW; F04A2BAID983E46 CRC64;

Query Match 7.5%; Score 92; DB 11; Length 427;
 Best Local Similarity 21.8%; Pred. No. 1.2; Mismatches 60; Indels 106; Gaps 12;
 Matches 53; Conservative 24; Mismatches 60; Indels 106; Gaps 12;

QY 44 YDLTRYLEHQLSLAGTYLNT---LGGP-----INP----- 72
 DB 204 YDPSSYNAHYLRNLFFPDGYDSLDPPASRVQEHILEVRRPHVLQGYFDESILLR 263
 QY 73 -----DENPRLGAEPLPRAT---VDEWWSLNDKLRITQWV 109
 DB 264 ELICWDLEDVLYFKLNARDSPVPRISGELYRATAMNLDVLYRHN--FEMKRV 321
 QY 110 YSHLCYLRGINQA-ATAEIRSL--LAHFCSTLQGLGSLA----- 153
 DB 322 F-----GREMARVAVELRQANEHMRHICIDGGAVGAELKDSAKL---PLGIKSI 373

DR EMBL: AE004483; AAC03843.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 733 AA; 81538 MW; 580F9D8BCB3909DB CRC64;

[illegible]

Search completed: March 18, 2002, 09:39:15
Job time: 531 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: March 18, 2002, 09:28:54 : Search time 55.47 Seconds
(without alignments)
300,460 Million cell updates/sec

Title: US-09-931-704-2
Perfect score: 1226
Sequence: 1 MDLRAGDSWGLACLTIVL.....KKKKMPAAVTLHGAGHF 225

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A.Geneseq_1101.*
1: /SID2/gcgdata/geneseq/geneseq/AA1980.DAT.*
2: /SID2/gcgdata/geneseq/geneseq/AA1981.DAT.*
3: /SID2/gcgdata/geneseq/geneseq/AA1982.DAT.*
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21: /SID2/gcgdata/geneseq/geneseq/AA2000.DAT.*
22: /SID2/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	AAW29715	Human neurotrophic
2	1226	100.0	225	AAW56141	Amino acid sequenc
3	1226	100.0	225	AAW94466	Human cardiotoxiph
4	1226	100.0	225	AAW7813	Human NNT-1 protei
5	1226	100.0	225	AAW63543	Amino acid sequenc
6	1226	100.0	225	AAW25831	Human protein sequ
7	1214	99.0	223	AAW29716	Human cardiotoxiph
8	1193	97.3	225	AAW29716	Mouse neurotrophic
9	1193	97.3	225	AAW56142	Amino acid sequenc
10	1193	97.3	225	AAW7814	Murine NNT-1 prote
11	1169	95.4	215	AAW19586	Human interleukin-

12	1136	92.7	215	21	AAW19587	Murine interleukin-
13	885	72.2	164	22	AAW20115	Protein #6549 enco
14	885	72.2	164	22	AAW34012	Protein #8049 enco
15	162.5	13.3	208	20	AAW09197	Human DNAX interle
16	160	13.1	203	16	AAW09196	Human DNAX interle
17	118.5	9.7	203	16	AAW83965	Mouse cardiac hype
18	118.5	9.7	203	17	AAW88204	Human cardiotoxiph
19	118.5	9.7	203	18	AAW29237	Murine cardiotoxiph
20	96.5	7.9	243	22	AAW20277	Human interleukin
21	92	7.5	332	21	AAW22132	Human interleukin
22	92	7.5	332	21	AAW40321	Human interleukin
23	91.5	7.5	201	16	AAW83967	Human cardiac hype
24	91.5	7.5	201	16	AAW29238	Human cardiac hype
25	91.5	7.5	201	16	AAW06490	Human tumour-assoc
26	91.5	7.5	201	21	AAW27662	Human protein PRO8
27	91.5	7.5	201	21	AAW13004	Human cardiotoxiph
28	91.5	7.5	201	21	AAW93697	Amino acid sequenc
29	91.5	7.5	201	21	AAW87818	Human cardiotoxiph
30	91.5	7.5	201	22	AAW50994	Human PRO882 prote
31	91	7.4	195	14	AAW34432	Sequence of growth
32	91	7.4	195	14	AAW83337	Chicken ciliary ne
33	91	7.4	242	22	AAW20275	Human interleukin
34	89.5	7.3	771	20	AAW34574	Human interleukin
35	89.5	7.3	766	20	AAW34431	Porphyromonas ging
36	85.5	7.0	429	12	AAW10976	Porphyromonas ging
37	84.5	6.9	1473	22	AAW07658	Polylhydroxalkanoa
38	84	6.9	200	19	AAW37931	Human G-protein co
39	83.5	6.8	310	20	AAW87993	Amino acid sequenc
40	83.5	6.8	399	20	AAW34543	A human MCG4 prote
41	83.5	6.8	450	20	AAW34409	Porphyromonas ging
42	82.5	6.7	582	14	AAW41000	Porphyromonas ging
43	82.5	6.7	1189	20	AAW15217	Human brain CDNA c
44	82	6.7	200	15	AAW53425	Human Hairless W11
45	82	6.7	200	20	AAW83340	Human/rat chimeric

ALIGNMENTS

RESULT 1

ID AAW29715 standard; Protein: 225 AA.

AC AAW29715;

DT 09-NOV-1998 (first entry)

DE Human neurotrophic factor NNT-1.

XX NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant;
XX Alzheimer's disease; Parkinson's disease; Huntington's d disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndr; her;

KW peripheral neuropathy; dystrophy; neural retina degene; ition;
KW common variable immunodeficiency; CVID; selective IGA d; deficiency;
KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; au; septic;
therapy.

KW hypogammaglobulinaemia; X-linked agammaglobulinaemia; au; septic;
therapy.

KW Homo sapiens.

OS Homo sapiens.

FT Key Location/Qualifiers
FT Peptide 1..27
FT Protein /label= Sig-peptide
FT 28..225
FT /label= Mat-protein

FN W09833922-AL.

PD 06-AUG-1998.

PF 02-FEB-1998;

PR 30-JAN-1998;

PR 03-FEB-1997;

Murine interleukin-
Protein #6549 enco
Protein #8049 enco
Human DNAX interle
Human DNAX interle
Mouse cardiac hype
Human cardiotoxiph
Murine cardiotoxiph
Human interleukin
Human interleukin
Human cardiac hype
Human cardiac hype
Human tumour-assoc
Human protein PRO8
Human cardiotoxiph
Amino acid sequenc
Human cardiotoxiph
Human PRO882 prote
Sequence of growth
Chicken ciliary ne
Human interleukin
Porphyromonas ging
Porphyromonas ging
Polylhydroxalkanoa
Human G-protein co
Amino acid sequenc
A human MCG4 prote
Porphyromonas ging
Porphyromonas ging
Human brain CDNA c
Human Hairless W11
Human/rat chimeric
Modified ciliary n

XX (AMGE-) AMGEN INC.
 XX Chang M, Elliot GS, Sarmiento U, Senaldi G;
 PI WPI: 1998-437475/37.
 DR N-PSDB; AAV47510-11.
 XX

PT Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 XX immunological diseases or inflammation, also as vaccine adjuvant
 PS
 XX
 PS Claim 12; Fig 3; 120pp; English.

CC This is the amino acid sequence of a novel neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or
 CC T cells. It was deduced from isolated cDNA (see AAV47510) and
 CC genomic DNA (see AAV47511) clones. Vectors containing the cDNA or
 CC of NNT-1 polypeptides. These are used for use in the production
 CC or immunological diseases, specifically Alzheimer's, Parkinson's
 CC or Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC selective IgA deficiency, hypogammaglobulinemia and X-linked
 CC agammaglobulinemia (claimed) but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. In addition, cells that have been engineered to
 CC express NNT-1 can be implanted, or nucleic acids are delivered in
 CC gene therapy vectors.
 XX
 SQ Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 5.6e-120;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDLRAGDSWGMACLCCTVLMHLPAYPALNRTGDPGSPISQKTYDLYRLYEHQSLAGT 60
 DB 1 mdlragswgmactclvtlwhlpaypalnrtgdp9p9pslqkydlyrlyehqslagt 60
 OY 61 YLNYIGPPFNEDPNPRIGAEETLPRAVDLEWRSINDKRLTLQWYEAESHLLCYRLG 120
 DB 61 ylnyigppfnedpnprigaeetlpratvdlewrsindkrltlqwyeyashllcylrgl 120
 OY 121 NROAATAELRRSLAHFCTSLGSLGSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 DB 121 nrgaataelrrslahfctslgslgslagvmaalgyplpplpcteptwtpgpahsdflq 180
 OY 181 KMDPFLLKELQTLWMSAKDENRLKKMKQPPAAAVTLHLGAHGF 225
 DB 181 kmddfllkeltqlwmsakdenrlkkmkppaaavtlhlghgaf 225

RESULT 2
 AAM56141
 ID AAM56141 standard; Protein; 225 AA.
 XX
 AC AAM56141;
 XX
 DT 13-JUL-1998 (first entry)
 DE Amino acid sequence of human neurotrophic factor NNT-1.
 XX
 DE Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KW treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..27
 FT Protein /note="signal peptide"
 FT 28..225
 XX /note="mature protein"
 XX
 XX US5741772-A.
 XX
 XX PD 21-APR-1998.
 XX
 XX PE 03-FEB-1997; 97US-0792019.
 XX
 XX PR 03-FEB-1997; 97US-0792019.
 XX
 XX PA (AMGE-) AMGEN INC.
 XX
 XX PI Chang M;
 XX
 XX DR WPI: 1998-260526/23.
 XX
 XX DR N-PSDB; AAV22652.
 XX

PT Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
 PT useful for stimulating growth of motor and sympathetic neurons
 XX
 XX Claim 1; Fig 3; 41pp; English.

CC The present sequence represents a human neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC stroke and various degenerative disorders affecting vision.
 XX
 SQ Sequence 225 AA;

Query Match 100.0%; Score 1226; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 5.6e-120;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDLRAGDSWGMACLCCTVLMHLPAYPALNRTGDPGSPISQKTYDLYRLYEHQSLAGT 60
 DB 1 mdlragswgmactclvtlwhlpaypalnrtgdp9p9pslqkydlyrlyehqslagt 60
 OY 61 YLNYIGPPFNEDPNPRIGAEETLPRAVDLEWRSINDKRLTLQWYEAESHLLCYRLG 120
 DB 61 ylnyigppfnedpnprigaeetlpratvdlewrsindkrltlqwyeyashllcylrgl 120
 OY 121 NROAATAELRRSLAHFCTSLGSLGSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 DB 121 nrgaataelrrslahfctslgslgslagvmaalgyplpplpcteptwtpgpahsdflq 180
 OY 181 KMDPFLLKELQTLWMSAKDENRLKKMKQPPAAAVTLHLGAHGF 225
 DB 181 kmddfllkeltqlwmsakdenrlkkmkppaaavtlhlghgaf 225

RESULT 3
 AAM94466
 ID AAM94466 standard; Protein; 225 AA.
 XX
 AC AAM94466;
 XX
 DT 22-APR-1999 (first entry)
 DE Human cardiotrophin-like cytokine protein.
 XX
 DE Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;
 KW CILC; IL-6; diagnosis; detection; immune system-related disorder;
 KW cancer; cardiac disorder; heart failure; hypertension; cancer;
 KW autoimmune disorder; infection.

XX	OS	Homo sapiens.	Location/Qualifiers
XX	XX	Key	1..27
PH	FT	Peptide	/label= signal
FT	FT	Protein	28..225
FT	FT	Protein	/label= Cardiotrophin-like_cytokine
FT	FT	Domain	74..79
FT	FT	Domain	/label= CD-I
FT	FT	Domain	/note= "conserved domain"
FT	FT	Domain	150..156
FT	FT	Domain	/label= CD-II
FT	FT	Domain	/note= "conserved domain"
FT	FT	Domain	194..198
FT	FT	Domain	/label= CD-III
FT	FT	Domain	/note= "conserved domain"
XX	XX	MO9900415-A1.	
PD	PD	07-JAN-1999.	
XX	XX	29-JUN-1998:	98MO-US13129.
XX	XX	30-JUN-1997:	97US-0051311.
XX	XX	(HUMA-) HUMAN GENOME SCI INC.	
XX	XX	Ruben SM, Shi Y:	
XX	XX	WPI: 1999-095678/08.	
DR	DR	N-PSDB: AAX16161.	
XX	XX	New isolated cardiotrophin-like cytokine nucleic acid - used to develop products for treating cardiac and immune system disorders and e.g. heart failure, hypertension, cancers, autoimmune disorders and infections	
PS	PS	Claim 1; Fig 1; 103pp; English.	
XX	XX	The present invention relates to a novel cardiotrophin-like cytokine (CIC) protein which is a member of the interleukin 6 (IL-6) cytokine family. The present sequence represents the human CIC protein in the present invention also describes screening methods for identifying agonists and antagonists of CIC activity, as well as methods for detecting cardiac and immune system-related disorders and therapeutic methods for treating cardiac and immune system-related disorders e.g heart failure, hypertension, cancers, autoimmune disorders and infections.	
XX	XX	Sequence 225 AA:	
XX	XX	Query Match	100.0%: Score 1226; DB 20; Length 225;
XX	XX	Best Local Similarity	100.0%: Pred. No. 5,6e-120; Indels 0; Gaps 0
XX	XX	Matches 225: Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	QY	1 MDKAGSGWMLACTCTVIMHLPAVPALNRTGDPGPGPSIOKTYDILTRYLHQRLSLAGT	60
DB	DB	1 MDLRAAGSGWMLACTCTVIMHLPAVPALNRTGDPGPGPSIOKTYDILTRYLHQRLSLAGT	60
QY	QY	61 YLNTYIGPPNPPNPRLGAETLPRATVLEWRSLSNDKLRITONVEASHLLCYRGL	120
DB	DB	61 YLNTYIGPPNPPNPRLGAETLPRATVLEWRSLSNDKLRITONVEASHLLCYRGL	120
QY	QY	121 NROQATAEILRSIAHCTSLQGLGSIACVMAALGYPLPOLPCTGPTPTWPGPAHSDPQ	180
DB	DB	121 NROQATAEILRSIAHCTSLQGLGSIACVMAALGYPLPOLPCTGPTPTWPGPAHSDPQ	180
QY	QY	181 KMDDFWILKELOTWLMRSAGDKFNLRKKKKMPAAATVTLHGANGF	225
DB	DB	181 KMDDFWILKELOTWLMRSAGDKFNLRKKKKMPAAATVTLHGANGF	225

RESULT 4
ID AAY87813 standard; protein; 225 AA.
XX AAY87813;
XX 24-AUG-2000 (first entry)
XX Human NNT-1 protein.
XX
XX NNT-1; human; neurotrophic factor; neurotrophic; neurotrophic; treatment;
XX anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
XX nervous system degeneration; Alzheimer's disease; Parkinson's disease;
XX amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
XX Huntington's disease; peripheral neuropathy; neural retinal degeneration;
XX retinopathy; immune disorder; hematopoietic disorder.
XX Homo sapiens.
OS
PN US6054294-A.
PD 25-APR-2000.
XX
XX 12-DEC-1997; 97US-0988819.
PE 03-FEB-1997; 97US-0792019.
PR (AMGE-) AMGEN INC.
PA
PI Chang M.
PI
PI WPI; 2000-338492/29.
DR N-PSDB; AAA39481.
XX
XX New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuronal cell damage
PT
XX
XX Claim 1c; Fig 3; 42pp; English.
XX
XX This invention describes a novel nucleic acid molecule (i) encoding a
PS novel neurotrophic factor (NNT-1) (ii) which has nothropic
CC novel neurotrophic factor (NNT-1) (iii) which has nothropic and
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC ophthalmological activity. (i) is useful for producing NNT-1
CC ophthalmological activity. (i) is useful for producing NNT-1
CC polypeptides which are useful for treating patients in whom various
CC cells of the central, autonomic, or peripheral nervous system have
CC degenerated and/or have been damaged by congenital disease, trauma,
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC disease, peripheral neuropathy or degeneration of the neural retina such
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC night blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (i) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence represents the human NNT-1 protein described in
CC the method of the invention.
CC
XX
XX Sequence 225 AA;
SQ

Query Match 100.0%; Score 1226; DB 21; Length 225;
Best Local Similarity 100.0%; Pred. No. 5,6e-120; Includ. 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 0;

1 MDRACDMSGMLACTCTVLMHPPAYPALNRGGDPGPGSIKTYDLTRYLEHOLRSIAGT 60
1 mdrlagsgwmlactctvlmhpavpalnrtdgpppsiktydlrlehlrsiag 60
Db

OY 181 KMDFWLLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAGHF 225
 |||
 Db 181 kmddfllkqlgwlsrskdfrlkkmqppaasvllhleahtf 225

RESULT 10

AAV87814 standard; Protein; 225 AA.

AAV87814;

24-AUG-2000 (first entry)

Murine NMT-1 protein.

NMT-1; neurotrophic factor; nootropic; neuroprotective; treatment; anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological; nervous system degeneration; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine; Huntington's disease; peripheral neuropathy; neural retina degeneration; retinopathy; immune disorder; hematopoietic disorder.

Mus sp.

US6054294-A.

25-APR-2000.

12-DEC-1997; 97US-0988819.

03-FEB-1997; 97US-0792019.

(AMGE-) AMGEN INC.

Chang M;

WPI: 2000-338492/29.

N-PSDB: AAA39483.

New nucleic acids encoding neurotrophic factors useful for stimulating growth of motor or sympathetic neurons for treating neuron cell damage

Claim 2b; Fig 5; 42pp; English.

This invention describes a novel nucleic acid molecule (I) encoding a novel neurotrophic factor (NMT-1) (II) which has nootropic, neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and ophthalmological activity. (I) is useful for producing NMT-1 polypeptides which are useful for treating patients in whom various cells of the central, autonomic, or peripheral nervous system have degenerated and/or have been damaged by congenital disease, trauma, mechanical damage, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy and/or toxic agents. NMT-1 proteins are used to treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral neuropathy induced by diabetes or other metabolic disorders, and/or dystrophies or degeneration of the neural retina such as retinitis pigmentosa, drug-induced retinopathies, stationary forms of night blindness, progressive cone-rod degeneration, immune disorders and hemopoietic disorders. (I) is effective in treating neurological conditions and promotes neuron regeneration. Neural functions are effectively restored in patients suffering from various neurological disorders. This sequence represents the murine NMT-1 protein described in the method of the invention.

Sequence 225 AA;

Query Match 97.3%; Score 1193; DB 21; Length 225;
 Best Local Similarity 96.9%; Pred. No. 1,6e-116;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 1 MDLRAGDSWGMALACTCTVYMHLPAPVPAIMRTGPGPGPSIOKTVDFLTAI : LKSLAGT 60
 |||
 Db 1 mdlragswgmalcctvylhlpavpalnrtgpgpgpsiqktydltcy : lkslsgt 60
 OY 61 YLNIYIPPPENPEPPNPRIGAEFTLPRAVDLEWRSINDKRLQNEAYSLCLCYLGL 120
 |||
 Db 61 yllylpppennppnprlgaeflpratydvlewrsindkrlqneyeashllylgl 120
 OY 121 NROAATAELRSLAHFCTSLQGLGSLAGYMALGYPLQPGREPTWPGPAHSDFEQ 180
 |||
 Db 121 nrgaataelrslahfctslqglgslagymalgyplpdpjycepapghsdfelq 180
 OY 181 KMDFWLLKELQTLWMSAKDFNRLKKKQPPAAVTLHLGAGHF 225
 |||
 Db 181 kmddfllkqlgwlsrskdfrlkkmqppaasvllhleahtf 225

RESULT 11

AAV19586 standard; Protein; 215 AA.

AAV19586;

22-JAN-2001 (first entry)

Human interleukin-B60 (IL-B60).

Interleukin-B60; IL-B60; human; cytokine; cytokine-like factor-1;

haematopoietic; inflammation; antinflammatory; autoimmune disease;

therapy.

Homo sapiens.

key Location/Qualifiers

peptide 1..17

protein /label= signal_peptide

18..215

/label= Mature-protein

WO200053631-A1.

14-SEP-2000.

09-MAR-2000; 2000MO-US06182.

11-MAR-1999; 99US-0267901.

(SCHE) SCHERING CORP.

Oppmann B, Timans JC, Kastelein RA, Bazan JF;

WPI: 2000-587426/55.

N-PSDB: AAA88546.

Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,

polypeptides, and nucleic acids, useful in research, diagnosis and for

treating inflammatory and autoimmune disorders.

Claim 1; Page 15-16; 97pp; English.

The present sequence is that of human interleukin-B60 (IL-B60), a novel, small soluble cytokine-like protein that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-B60 may have either stimulatory or inhibitory effects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist or antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see AAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological

CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.
XX
SQ Sequence 215 AA;

Query Match 95.4%; Score 1169; DB 21; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.8e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 MLCACITVLMHLPVAVPALNRTGDPGPGSPSTQKTYDITRYLEHOLRSLACTYLYNVLGPPN 70
DB 1 mlaclctvlwhlpavpalnrtgdpgpspstktydltrylehqjrsagtylnylgppn 60
QY 71 EPDFNPRLGAETLPRAVDLEWRSINDKRLTONVEAVSHLCTYLRGLNQAAATAEIR 130
DB 61 epdfnprrlgaetlpravtdelewrslndkrltongveavshlctylrglnqaaataelr 120
QY 131 RSLAHFCTSLGSLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDPWLKE 190
DB 121 rslahfctslgslisagvmaalgyplpqplpgteptwtpgpahsdfqkmdfwlke 180
QY 191 LQTWLMSAKDENRLLKKMQPPAAVTLHGAHGF 225
DB 181 lqtwlmsakdenrllkkmqppaavtlhghgf 215

RESULT 12
AAB19587
ID AAB19587 standard; Protein; 215 AA.
XX
AC AAB19587;
XX
DT 22-JAN-2001 (first entry)
XX
DE Mouse Interleukin-B60 (IL-B60).
XX
KW Interleukin-B60; IL-B60; mouse; cytokine; cytokine-like factor-1;
KW hematopoietic; inflammation; antiinflammatory; autoimmune disease;
XX
OS Mus musculus.

Key Location/Qualifiers
FH Peptide 1..17
FT /label= Signal_peptide
FT 18..215
FT Protein /label= Mature-protein

WO200053631-A1.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06182.
XX
PR 11-MAR-1999; 99US-0267901.
XX
PA (SCHE) SCHERING CORP.

XX
PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;
XX
DR WPI: 2000-587426/55.
XX
DR N-PSDB: AAA88547.

XX
PT Cytokine-like factor 1 (CLF-1) and Interleukin (IL)-B60 complexes,
PT polypeptides, and nucleic acids, useful in research, diagnosis and for
PT treating inflammatory and autoimmune disorders -
XX
PS Claim 1; Page 17; 97pp; English.

XX
CC The present sequence is that of mouse interleukin-B60 (IL-B60), a
CC novel, small soluble cytokine-like protein that exhibits structural

CC motifs characteristic of a member of the long-chain cytokines, and
CC which shows homology to granulocyte colony stimulating factor and
CC interleukin-6. IL-60B may have either stimulatory or inhibitory
CC effects on hematopoietic cells, including e.g. lymphoid cells,
CC such as T-cells, B-cells, natural killer cells, macrophages,
CC dendritic cells, hematopoietic progenitors, etc. Methods are
CC provided for modulating the physiology or development of a cell or
CC tissue culture cells by contacting the cell with an agonist or
CC antagonist of IL-B60 or an agonist of antagonist of a cell or
CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
CC AAB19587). The IL-B60/CLF-1 cytokine serves as a key physiological
CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.
XX
SQ Sequence 215 AA;

Query Match 92.7%; Score 1136; DB 21; Length 15;
Best Local Similarity 96.7%; Pred. No. 1.3e-110;
Matches 208; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 11 MLCACITVLMHLPVAVPALNRTGDPGPGSPSTQKTYDITRYLEHOLRSLACTYLYNVLGPPN 70
DB 1 mlaclctvlwhlpavpalnrtgdpgpspstktydltrylehqjrsagtylnylgppn 60
QY 71 EPDFNPRLGAETLPRAVDLEWRSINDKRLTONVEAVSHLCTYLRGLNQAAATAEIR 130
DB 61 epdfnprrlgaetlpravtdelewrslndkrltongveavshlctylrglnqaaataelr 120
QY 131 RSLAHFCTSLGSLGSIAGVMAALGYPLPQPLPGTEPTWTPGPAHSDFLQKMDPWLKE 190
DB 121 rslahfctslgslisagvmaalgyplpqplpgteptwtpgpahsdfqkmdfwlke 180
QY 191 LQTWLMSAKDENRLLKKMQPPAAVTLHGAHGF 225
DB 181 lqtwlmsakdenrllkkmqppaavtlhghgf 215

RESULT 13
AAM20115
ID AAM20115 standard; Protein; 164 AA.
XX
AC AAM20115;
XX
DT 12-OCT-2001 (first entry)
XX
DE Peptide #6549 encoded by probe for measuring cervical gene expression.
XX
KW Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer.
XX
KW Homo sapiens.

XX
PD WO200157278-A2.
XX
PF 09-AUG-2001.
XX
PI 30-JAN-2001; 2001WO-US00670.

XX
PR 04-FEB-2000; 2000US-0180312.
XX
PR 26-MAY-2000; 2000US-0207456.
XX
PR 30-JUN-2000; 2000US-0608408.
XX
PR 03-AUG-2000; 2000US-0632366.
XX
PR 21-SEP-2000; 2000US-0234687.
XX
PR 27-SEP-2000; 2000US-0236359.
XX
PR 04-OCT-2000; 2000GB-0024263.

XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DK;
XX
DR WPI: 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human cervical epithelial cells -
 XX

PS Claim 27; SEQ ID NO 24941; 487bp; English.

CC The present invention relates to human single exon nucleic acid probes
 CC (SENP: see A110068-A118459). The present sequence is a peptide encoded
 CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
 CC can be used to produce a single exon microarray, which can be used for
 CC measuring human gene expression in a sample derived from human cervical
 CC epithelial cells. By measuring gene expression, the probes are therefore
 CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

CC Sequence 164 AA:

Query Match 72.2%; Score 885; DB 22; Length 164;
 Best Local Similarity 99.4%; Pred. No. 1.6e-84;
 Matches 163; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 62 LNYGPPFNEPFPRLGAEPLPRATVDLEWRSINDKRLQWNEAVSHLCYLRGLN 121
 Db 1 lnygppfnepfprrlgaeplpratvdlewrsindkrlrltqneyeshlcylyrqln 60
 QY 122 RQATTAELRRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPOTPTWTPGPAHSDFLQK 181
 Db 61 rqaataelrrslahfctslqglgsiagvmaalgyplpqpplpoptwtpgpaahsdflqk 120
 QY 182 MDFFWLKELQTLWLRSAKDFNRLKKMQPPAAAVTLHGAGHF 225
 Db 121 mdffwlkeltlwlrtsakdfnrllkkmqppaavtlhlgahgf 164

RESULT 14

AAM34012
 ID AAM34012 standard; Protein: 164 AA.

XX AAM34012;

DT 17-OCT-2001 (first entry)

DE Peptide #8049 encoded by probe for measuring placental gene expression.

XX Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.

XX Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0633366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MODE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for
 PT analyzing gene expression in human placenta -
 XX

PS Claim 27; SEQ ID NO 34281; 654bp; English.

CC The present invention relates to single exon nucleic acid probes (SENP:
 CC see A1131315-A1157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders.

XX Sequence 164 AA:

Query Match 72.2%; Score 885; DB 22; Length 164;
 Best Local Similarity 99.4%; Pred. No. 1.6e-84;
 Matches 163; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 62 LNYGPPFNEPFPRLGAEPLPRATVDLEWRSINDKRLQWNEAVSHLCYLRGLN 121
 Db 1 lnygppfnepfprrlgaeplpratvdlewrsindkrlrltqneyeshlcylyrqln 60
 QY 122 RQATTAELRRSLAHFCTSLQGLGSIAGVMAALGYPLPQPLPOTPTWTPGPAHSDFLQK 181
 Db 61 rqaataelrrslahfctslqglgsiagvmaalgyplpqpplpoptwtpgpaahsdflqk 120
 QY 182 MDFFWLKELQTLWLRSAKDFNRLKKMQPPAAAVTLHGAGHF 225
 Db 121 mdffwlkeltlwlrtsakdfnrllkkmqppaavtlhlgahgf 164

RESULT 15

AAV09197
 ID AAV09197 standard; Protein: 208 AA.

XX AAV09197;

DT 20-JUL-1999 (first entry)

DE Human DMAX Interleukin-40 (DIL-40) alternative sequence.

XX DMAX interleukin-40; DIL-40; activation regulation; development;
 KW differentiation; hematopoietic; neural cell; drug targeting;
 XX immunological condition.

OS Homo sapiens.

PN WO9919491-A2.

PD 22-APR-1999.

PF 13-OCT-1998; 98WO-US20932.

PR 14-OCT-1997; 97US-0950238.

PA (SCHE) SCHERING CORP.

PI Bazan JF, Kastelein RA;

DR WPI, 1999-312475/26.

DR N-PSDB; AAX60797.

PT New human DMAX Interleukin-40 (DIL-40) polypeptide and antagonists

PS Claim 1; Page 10-11; 76pp; English.

CC The invention relates to a human DMAX interleukin-40 (DIL-40) protein.
 CC Host cells containing a vector comprising the DIL-40 nucleic acid can be
 CC used for the recombinant expression of the protein. The DIL-40 protein,
 CC gene and antibody are useful for regulating activation, development
 CC differentiation and function of various cell types, including
 CC hematopoietic or neural cells. The antibodies may be antagonists, and

Mon Mar 18 11:23:39 2002

us-09-931-704-2.ra1

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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:28:54 ; Search time 30.45 seconds
(without alignments)
166.280 Million cell updates/sec

Title: US-09-931-704-2
Perfect score: 1226
Sequence: 1 MDLRAGDSWGMALCTVLM.....KKKKPPAAAVTLHGANGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues
Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/prodata/2/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/2/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/2/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/2/1aa/PCITUS.COMB.pep.*
6: /cgn2_6/prodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1226	100.0	225	US-08-792-019B-2	Sequence 2, Appli
2	1226	100.0	225	US-09-106-182-2	Sequence 2, Appli
3	1226	100.0	225	US-08-988-819-2	Sequence 2, Appli
4	1226	100.0	225	US-09-016-534-2	Sequence 5, Appli
5	1193	97.3	225	US-08-792-019B-5	Sequence 5, Appli
6	1193	97.3	225	US-08-988-819-5	Sequence 5, Appli
7	1193	97.3	225	US-09-016-534-5	Sequence 5, Appli
8	124.5	10.2	203	US-09-106-182-3	Sequence 3, Appli
9	118.5	9.7	203	US-08-233-609-3	Sequence 3, Appli
10	118.5	9.7	203	US-08-444-083-3	Sequence 3, Appli
11	118.5	9.7	203	US-08-286-304-3	Sequence 3, Appli
12	118.5	9.7	203	US-08-442-745-3	Sequence 3, Appli
13	118.5	9.7	203	US-08-443-129-3	Sequence 3, Appli
14	118.5	9.7	203	US-08-443-952-3	Sequence 3, Appli
15	118.5	9.7	203	US-08-443-130-3	Sequence 3, Appli
16	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
17	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
18	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
19	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
20	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
21	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
22	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
23	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
24	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
25	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
26	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli
27	118.5	9.7	203	US-08-898-911-3	Sequence 3, Appli

28	91.5	7.5	201	4	US-09-016-534-11	Sequence 11, Appli
29	91.5	7.5	201	5	PCT-US95-04467-8	Sequence 8, Appli
30	91	7.4	195	1	US-07-959-284-5	Sequence 5, Appli
31	91	7.4	195	2	US-08-308-736A-5	Sequence 2, Appli
32	91	7.4	195	5	PCT-US92-08258-2	Sequence 2, Appli
33	91	7.4	195	5	PCT-US93-09649A-5	Sequence 5, Appli
34	91	7.4	195	5	PCT-US93-09649-5	Sequence 5, Appli
35	85.5	7.0	560	2	US-08-756-317-11	Sequence 11, Appli
36	84	6.9	200	4	US-08-949-155-4	Sequence 4, Appli
37	82.5	6.7	582	2	US-08-422-699A-9	Sequence 9, Appli
38	82.5	6.7	582	2	US-08-422-706B-9	Sequence 9, Appli
39	82	6.7	200	1	US-07-959-284-8	Sequence 8, Appli
40	82	6.7	200	2	US-08-308-736A-8	Sequence 8, Appli
41	82	6.7	200	2	PCT-US93-09649A-8	Sequence 8, Appli
42	82	6.7	200	5	PCT-US93-09649-8	Sequence 8, Appli
43	81	6.6	200	1	US-07-959-284-6	Sequence 6, Appli
44	81	6.6	200	2	US-08-308-736A-6	Sequence 6, Appli
45	81	6.6	200	5	PCT-US93-09649A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-792-019B-2
Sequence 2, Appli Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ. ID NO. 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-2
Query Match 100.0%; Score 1226; DB 1; Length 225;
Best local Similarity 100.0%; Pred. No. 3,1e-129; Indels 0; Gaps 0;
Matches 225; Conservative 0; Mismatches 0;
QY 1 MDLRAGDSWGMALCTVLMHPALNRTGDPGSPSIQKYVTLRLTFLR...LISLIGT 60
DQ 1 MDLRAGDSWGMALCTVLMHPALNRTGDPGSPSIQKYVTLRLTFLR...LISLIGT 60
QY 61 YLNTLGPFPPFPNPPRGAETLPRAVDLEWRSNDKRLTQNTENAVSHLLCTRL 120
DQ 61 YLNTLGPFPPFPNPPRGAETLPRAVDLEWRSNDKRLTQNTENAVSHLLCTRL 120
QY 121 NROATAELRLSLAHFTSLGSLGSLAGVMAALGYPLDPLPGETEPFWP...VHSDPLD 180
DQ 121 NROATAELRLSLAHFTSLGSLGSLAGVMAALGYPLDPLPGETEPFWP...VHSDPLD 180

Db 121 NRQAATAELRSLAHCTSLQGLLSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225
 Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225

RESULT 2

US-09-106-182-2
 : Sequence 2, Application US/09106182
 : Patent No. 6046035
 : GENERAL INFORMATION:
 : APPLICANT: Shi, Yangu
 : APPLICANT: Ruben, Steve
 : TITLE OF INVENTION: Cardiotrophin-Like Cytokine
 : NUMBER OF SEQUENCES: 24
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Human Genome Sciences, Inc
 : STREET: 9410 Key West Ave
 : CITY: Rockville
 : STATE: MD
 : COUNTRY: US
 : ZIP: 20850
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/106,182
 : FILING DATE: Herewith
 : CLASSIFICATION:
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 60/051,053
 : FILING DATE: 30-JUN-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Brookes, A. Anders
 : REGISTRATION NUMBER: 36,373
 : REFERENCE/DOCKET NUMBER: PF385
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 301-309-8504
 : TELEFAX: 301-309-8439
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 225 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-09-106-182-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-129;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGMACLCYVLMHLPVAVPALNRTGDPGPGPSIOKTYDTRYLEHQLSLAGT 60
 Db 1 MDLRAGDSWGMACLCYVLMHLPVAVPALNRTGDPGPGPSIOKTYDTRYLEHQLSLAGT 60
 QY 61 YLNYIGPPFNEPDNPRLGAETLPRAIVDLEWWSLNKRLTONYEAYSHLLCYLGL 120
 Db 61 YLNYIGPPFNEPDNPRLGAETLPRAIVDLEWWSLNKRLTONYEAYSHLLCYLGL 120
 QY 121 NRQAATAELRSLAHCTSLQGLLSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 Db 121 NRQAATAELRSLAHCTSLQGLLSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225
 Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225

RESULT 3

US-08-988-819-2
 : Sequence 2, Application US/08988819
 : Patent No. 6054294
 : GENERAL INFORMATION:
 : APPLICANT: CHANG, MING-SHI
 : TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: AMGEN INC.
 : STREET: ONE AMGEN CENTER DRIVE
 : CITY: THOUSAND OAKS
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 91320
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : OPERATING SYSTEM: IBM PC compatible
 : SOFTWARE: Patent Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/988,819
 : FILING DATE: 12-DEC-1997
 : CLASSIFICATION: 536
 : PRIORITY APPLICATION DATA:
 : APPLICATION NUMBER: US 08/792,019
 : FILING DATE: 03-FEB-1997
 : ATTORNEY/AGENT INFORMATION:
 : NAME: COOK, ROBERT R.
 : REGISTRATION NUMBER: 31,602
 : REFERENCE/DOCKET NUMBER: A-442A
 : INFORMATION FOR SEQ ID NO: 2:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 225 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: protein
 : US-08-988-819-2

Query Match 100.0%; Score 1226; DB 3; Length 225;
 Best Local Similarity 100.0%; Pred. No. 3.1e-129;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDLRAGDSWGMACLCYVLMHLPVAVPALNRTGDPGPGPSIOKTYDTRYLEHQLSLAGT 60
 Db 1 MDLRAGDSWGMACLCYVLMHLPVAVPALNRTGDPGPGPSIOKTYDTRYLEHQLSLAGT 60
 QY 61 YLNYIGPPFNEPDNPRLGAETLPRAIVDLEWWSLNKRLTONYEAYSHLLCYLGL 120
 Db 61 YLNYIGPPFNEPDNPRLGAETLPRAIVDLEWWSLNKRLTONYEAYSHLLCYLGL 120
 QY 121 NRQAATAELRSLAHCTSLQGLLSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 Db 121 NRQAATAELRSLAHCTSLQGLLSIAGVMAALGYPLPGLPCTEPTWTPGPAHSDFLQ 180
 QY 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225
 Db 181 KMDDFWLKELQTLWLRSAKDFNRLKKMKOPPAAVTLHGAHGF 225

Mon Mar 18 11:23:39 2002

us-09-931-704-2.ral

Page 3

ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-534-2

Query Match 100.0%; Score 1226; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 3, 1e-129;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 1 MDLRAGDSMGLACTVIMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 1 YLNTLGPPFNEPDPNPRIGAEITLPRAIVDLEWRSNDKRLTONYEAVSHLLCYLRGL 120
DB 61 YLNTLGPPFNEPDPNPRIGAEITLPRAIVDLEWRSNDKRLTONYEAVSHLLCYLRGL 120
QY 121 NROAATAEELRSLAHFCTSLQGLGSIAGYMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180
DB 121 NROAATAEELRSLAHFCTSLQGLGSIAGYMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTWLMSAKDFNRLKKMKOPPAASVTLHLGAHGF 225
DB 181 KMDDFWLKELQTWLMSAKDFNRLKKMKOPPAASVTLHLGAHGF 225

RESULT 5
US-08-792-019B-5
Sequence 5, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-5

Query Match 97.3%; Score 1193; DB 1; Length 225;
Best Local Similarity 96.9%; Pred. No. 1, 5e-125;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
DB 1 MDLRAGDSMGLACTVIMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 1 YLNTLGPPFNEPDPNPRIGAEITLPRAIVDLEWRSNDKRLTONYEAVSHLLCYLRGL 120
DB 61 YLNTLGPPFNEPDPNPRIGAEITLPRAIVDLEWRSNDKRLTONYEAVSHLLCYLRGL 120
QY 121 NROAATAEELRSLAHFCTSLQGLGSIAGYMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180
DB 121 NROAATAEELRSLAHFCTSLQGLGSIAGYMAALGYPLPQPLGTEPTWTPGPAHSDFLQ 180
QY 181 KMDDFWLKELQTWLMSAKDFNRLKKMKOPPAASVTLHLGAHGF 225
DB 181 KMDDFWLKELQTWLMSAKDFNRLKKMKOPPAASVTLHLGAHGF 225

RESULT 6
US-08-988-819-5
Sequence 5, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-988-819-5

Query Match
Best Local Similarity 97.3%; Score 1193; DB 3; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLCCTVLMHLPAPVALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
DB 1 MDLRAGDSWGMACLCCTVLMHLPAPVALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 61 YLNYLGPPNEDPFPRLGATLPRATVDEWVRSNDKRLQNEEAVSHLLCYLRL 120
DB 61 YLNYLGPPNEDPFPRLGATLPRATVDEWVRSNDKRLQNEEAVSHLLCYLRL 120
QY 121 NROAATAELRSLAHFCTSLQGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
DB 121 NROAATAELRSLAHFCTSLQGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
QY 181 KMDPFWLKELOTWLRSAKDENLKKKMPAPAAVTLHGANGF 225
DB 181 KMDPFWLKELOTWLRSAKDENLKKKMPAPAAVTLHGANGF 225

RESULT 7

US-09-016-534-5
Sequence 5, Application US/09016534
Patent No. 6143874

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
APPLICANT: ELLIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-016-534-5

Query Match
Best Local Similarity 97.3%; Score 1193; DB 4; Length 225;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMACLCCTVLMHLPAPVALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60

DB 1 MDLRAGDSWGMACLCCTVLMHLPAPVALNRTGDPGPGSIQKTYDLTRYLEHQLRSLAGT 60
QY 61 YLNYLGPPNEDPFPRLGATLPRATVDEWVRSNDKRLQNEEAVSHLLCYLRL 120
DB 61 YLNYLGPPNEDPFPRLGATLPRATVDEWVRSNDKRLQNEEAVSHLLCYLRL 120
QY 121 NROAATAELRSLAHFCTSLQGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
DB 121 NROAATAELRSLAHFCTSLQGLGSLAGVMAALGYPLPQPLGTEPTWTGPAHSDFLQ 180
QY 181 KMDPFWLKELOTWLRSAKDENLKKKMPAPAAVTLHGANGF 225
DB 181 KMDPFWLKELOTWLRSAKDENLKKKMPAPAAVTLHGANGF 225

RESULT 8

US-09-106-182-3

Sequence 3, Application US/09106182
Patent No. 6046035

GENERAL INFORMATION:

APPLICANT: Shi, Yangu
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF385
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-106-182-3

Query Match
Best Local Similarity 10.2%; Score 124.5; DB 3; Length 203;
Matches 50; Conservative 24; Mismatches 85; Indels 19; Gaps 5;

QY 40 IOKYDITRYLEHQLRSLAGTLYWVYLGPPNEDPFPRLGATLPRATVDEWVRS 96
DB 27 IROTHNLARLLTKYVADQLEHYVQGGEPFGCLGFSPPRLPLAGSGPAPSHAGLPV--- 83
QY 97 LNDKRLQNEEAVSHLLCYLRLNROA-----TAEIRSLAHFCTSLQGLGSLAGVMA 151
DB 84 ---SERLRQDAALSLALPALLDAVRROAELNRPRLRLSLRSLDARQVRAALGAAYETVL 140

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2002, 09:33:29 ; Search time 1350.94 Seconds

(without alignments)
10001.325 Million cell updates/sec

Title: US-09-931-704-4

Perfect score: 819
Sequence: 1 tattatttaagcttcgcgcg.....agccccagctcagctgtcgtt 819

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_om: *
20: em_or: *
21: em_ov: *
22: em_pat: *
23: em_ph: *
24: em_pl: *
25: em_ro: *
26: em_sts: *
27: em_sy: *
28: em_un: *
29: em_vi: *
30: em_htgo_hum: *
31: em_htgo_inv: *
32: em_htgo_rod: *
33: em_htg_hum: *
34: em_htg_inv: *
35: em_htg_rod: *
36: em_htg_other: *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	819	100.0	819	6	AR002597
2	819	100.0	819	10	AF176913
3	669.4	81.7	797	6	AR002595
4	669.4	81.7	797	9	AF176911
5	627	76.6	1689	9	AF172854
6	429.6	52.5	5087	6	AR002596
7	429.6	52.5	5087	6	AF176912
8	429.6	52.5	135116	2	AP002437
9	429.6	52.5	151441	2	AP003419
10	428	52.3	169144	2	AC005849
11	46.2	5.6	47958	2	AC091104
12	44.4	5.4	187727	2	AC021142
13	43.2	5.3	6803	9	HS868758
14	42.4	5.2	1357	9	AF035771
15	42.4	5.2	1524	9	AF004900
16	42.4	5.2	1578	9	HSU82108
17	42.4	5.2	1600	9	HSFKAI1MR
18	42.4	5.2	1642	6	AR070449
19	42.2	5.2	1901	5	GGTAMBI
20	42	5.1	63082	2	AC022663
21	40.8	5.0	123554	9	AB023049
22	40.8	5.0	200000	9	AP000512
23	40.6	5.0	114653	2	AC092411
24	40.4	4.9	6955	1	TFHIIIVB
25	40.4	4.9	188947	2	AC087455
26	40.2	4.9	167693	2	AC011639
27	40.2	4.9	180626	2	AC022824
28	40.2	4.9	184485	2	AC009679
29	40.2	4.9	193263	2	AC090971
30	40	4.9	1246	6	AX164174
31	39.2	4.8	105935	9	AL355802
32	39.2	4.8	170530	2	AL359977
33	39.2	4.8	192634	2	AC069466
34	38.8	4.7	160312	2	AP003500
35	38.8	4.7	161286	2	AC025120
36	38.6	4.7	70452	9	HSJ854E16
37	38.6	4.7	227531	2	AC015705
38	38.4	4.7	16124	1	AX024384
39	38.4	4.7	16124	6	AX024277
40	38.4	4.7	23404	1	SCI10A9
41	38.4	4.7	68750	1	AF210843
42	38.4	4.7	178597	2	AC063962
43	38.2	4.7	1970	5	AB001742
44	38.2	4.7	37770	9	AC010513
45	38.2	4.7	145133	2	AC013822

ALIGNMENTS

RESULT 1
AR002597 LOCUS AR002597 819 bp DNA
DEFINITION Sequence 4 from patent US 5741772.
ACCESSION AR002597
VERSION AR002597.1 GI:3964151
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 819)
AUTHORS Chang, M.
TITLES Neurotrophic factor NNT-1
JOURNAL Patent: US 5741772-A 4 21-APR-1998;
FEATURES
source location/Qualifiers
1..819
BASE COUNT 156 a 288 c 218 g 157 t
ORIGIN

PAT 1-DEC-1998


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QY 541 tgcataggagagcttggtaccactgcccagctctgcccagagctgagccagct 600
DB 541 tgcataggagagcttggtaccactgcccagctctgcccagagctgagccagct 600
QY 601 ggcacctgagccctgcccagagctgacctcccaagaatgagatcttgcctgtga 660
DB 601 ggcacctgagccctgcccagagctgacctcccaagaatgagatcttgcctgtga 660
QY 661 ggaactgagagcttggtacatgagcttcccaagaatgagatcttgcctgtga 720
DB 661 ggaactgagagcttggtacatgagcttcccaagaatgagatcttgcctgtga 720
QY 721 ggaactgagagcttggtacatgagcttcccaagaatgagatcttgcctgtga 780
DB 721 ggaactgagagcttggtacatgagcttcccaagaatgagatcttgcctgtga 780
QY 781 ccttaacccccacactccagagccagctgagctgtgct 819
DB 781 ccttaacccccacactccagagccagctgagctgtgct 819

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RESULT 3
AR002595 797 bp DNA PAT 04-DEC-1998
LOCUS Sequence 1 from patent US 5741772.
DEFINITION AR002595
ACCESSION AR002595
VERSION AR002595.1 GI:3964149
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 797)
AUTHORS Chang, M.
TITLES Neurotrophic factor NNT-1
JOURNAL Patent: US 5741772-A 1 21-APR-1998;
FEATURES
source 1.797
location/Qualifiers
BASE COUNT 139 a 297 c 218 g 143 t
ORIGIN

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Query Match 81.7%; Score 669.4; DB 6; Length 797;
Best Local Similarity 92.0%; Pred. No. 6e-143;
Matches 717; Conservative 0; Mismatches 61; Indels 1; Gaps 1;
QY 5 attaaagcttcgagagccgagctgagctccctcccaactccgagagcttggagagag 64
DB 1 attaaagcttcgagagccgagctgagctccctcccaactccgagagcttggagagag 60
QY 65 ccgagccgagccgagccgagccgagccgagccgagccgagccgagccgagccgag 124
DB 61 ccgagccgagccgagccgagccgagccgagccgagccgagccgagccgagccgag 119
QY 125 atgttagcttgacatgacagctgagctgagctccctcccaactccgagagcttcaatgc 184
DB 120 atgttagcttgacatgacagctgagctgagctccctcccaactccgagagcttcaatgc 179
QY 185 acagagagatccagagccctgagccctccatccagaaacataagctaccagctaacctg 244
DB 180 acagagagatccagagccctgagccctccatccagaaacataagctaccagctaacctg 239
QY 245 gagatacaactccgagctgagctgagctgagctgagctgagctgagctgagctgagct 304
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LOCUS Homo sapiens neurotrophin-1/B-cell stimulating factor-3 mRNA,
DEFINITION complete cds.
ACCESSION AF176911
VERSION AF176911.1 GI:6007640
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE 1 (bases 1 to 797)
AUTHORS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Senaldi, G., Varnum, B., Sarmiento, U., Lile, J.,
Scully, S., Guo, J., Elliott, G., McNinch, J., Shaklee, C.,
Freeman, D., Mann, F., Simonet, M.S., Boone, T., and Chang, M.S.
Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the
IL-6 family
Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-1146, (1999)
JOURNAL 99432254
MEDLINE 2 (bases 1 to 797)
AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lile, J.,
Scully, S., Guo, J., Elliott, G., McNinch, J., Shaklee, C.,
Mann, F., Simonet, M.S., Boone, T., and Chang, M.S.
Direct Submission
Submitted (11-AUG-1999) Angen, Inc., One Angen Center Drive,
Thousand Oaks, CA 91320, USA
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RESULT 6
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 ACCESSION AR002596
 VERSION AR002596.1 GI:3964150
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 5087)
 AUTHORS Chang, M.
 TITLE Neurotrophic factor NNT-1
 JOURNAL Patent: US 5741772-A 3 21-Apr-1998;
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 Best Local Similarity 90.4%; Pred. No. 2.5e-88;
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 ACCESSION AF176912
 VERSION AF176912.1 GI:6007642
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 5087)
 AUTHORS Senaldi, G., Varnum, B.C., Sarmiento, U., Starnes, C., Lille, J., Scully, S., Guo, J., Elliott, G., McMinch, J., Freeman, D., Boone, T., and Chang, M.S.
 TITLE Novel neurotrophin-1/B cell-stimulating factor-3: a cytokine of the IL-6 family
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (20), 11458-114 (1999)
 MEDLINE 99432254
 REFERENCE 2 (bases 1 to 5087)
 AUTHORS Senaldi, G., Varnum, B., Sarmiento, U., Lille, J., Starnes, C., Scully, S., Guo, J., Elliott, G., McMinch, J., Freeman, D., Boone, T., Mann, F., Simonet, S., Boone, T., and Chang, M.S.
 TITLE Direct Submission
 JOURNAL Submitted (11-AUG-1999) Amgen, Inc., One Amgen Center Drive, Thousand Oaks, CA 91320, USA
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 Query Match 52.5%; Score 429.6; DB 9; Length 5087;
 Best Local Similarity 90.4%; Pred. No. 2.5e-88;
 Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
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 Db 3363 AGCTGAACCTACTGCGGCCCTTTCACAGCAGCCAGACTTACCCCTCCGCGCTGGGG 3422
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QY	336	cagaactctgcgccagggccagcgtctcaactcttggaaagtgtgcgaagctctcaatgaagcgc	395						
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QY	396	tgcgcctgaaccagaactatgagcgctacagtcacctctgtgttactctgtctgtgcctca	455						
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QY	456	accgtgaagcttcacacagctgaactccgaagctgaagctgtggccactctctgtaccagctcc	515						
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QY	576	ctctgcacaggactatgagccagctctgtgcccctgtgcctgtgcccaagatgaactctctcaga	635						
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DEFINITION				HO sapiens chromosome 11 clone CTD-1337H24 map 114, WORKING DRAFT					
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ORGANISM		HO sapiens							
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homi							
AUTHORS		1 (bases 1 to 151441)							
TITLE		Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Honi,Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.							
JOURNAL		Direct Submission							
COMMENT		Submitted (16-MAR-2001) Masahira Hattori, The Institute of Physica and Chemical Research (RIKEN), Genomic Sciences Center (GSC): 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gs.c.riken.go.jp, URL:http://nbp.gs.c.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)							
		Genome Center							
		Center: RIKEN Genomic Sciences Center(GSC)							
		Center code: RIKEN							
		Web site: http://nbp.gs.c.riken.go.jp/							
		Contact: hattori@gs.c.riken.go.jp							
		Project Information							
		Center project name: HumDra11							
		Center clone name: CTD-1337H24							
		Summary Statistics							
		Sequencing vector: PCR products; 100% of read							
		Chemistry: Dye-terminator ET-amersham; 100% of reads							
		Assembly program: Phrap; version 0.990329							

Consensus quality: 140857 bases at least Q40
 Consensus quality: 144624 bases at least Q30
 Consensus quality: 146614 bases at least Q20
 Insert size: 147641; sum-of-contigs
 Quality coverage: 7.92x in Q20 bases, sum-of-

NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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6	46961	46840	contig of	4815	bp	in	length
7	51538	51437	contig of	4497	bp	in	length
8	55206	55105	contig of	4568	bp	in	length
9	60387	60296	contig of	4091	bp	in	length
10	65110	65009	contig of	4613	bp	in	length
11	69544	69443	contig of	4334	bp	in	length
12	74026	73925	contig of	4382	bp	in	length
13	77474	77574	contig of	3549	bp	in	length
14	82587	82587	contig of	4913	bp	in	length
15	82668	87865	contig of	5178	bp	in	length
16	87966	92070	contig of	4105	bp	in	length
17	92121	96078	contig of	3908	bp	in	length
18	96179	100630	contig of	4452	bp	in	length
19	100771	100356	contig of	2628	bp	in	length
20	103445	107845	contig of	4387	bp	in	length
21	107946	110195	contig of	2250	bp	in	length
22	110286	113148	contig of	2853	bp	in	length
23	1116349	116288	contig of	3057	bp	in	length
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26	123840	126208	contig of	2369	bp	in	length
27	126309	128205	contig of	1897	bp	in	length
28	128306	132675	contig of	4370	bp	in	length
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30	134411	137659	contig of	3289	bp	in	length
31	137800	139568	contig of	1787	bp	in	length
32	139687	141655	contig of	1969	bp	in	length
33	141756	143142	contig of	1387	bp	in	length
34	143423	144600	contig of	1358	bp	in	length
35	144701	146265	contig of	1155	bp	in	length
36	146366	147564	contig of	1199	bp	in	length
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38	149092	150119	contig of	1028	bp	in	length
39	150220	151441	contig of	1222	bp	in	length

NOTE: This is a 'working draft' sequence. It currently consists of 39 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will then be preserved.

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Query Match	Similarity	52.5%	Score	429.6	DB 2	Length	151441
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Matches	459	Conservative	0	Mismatches	49	Indels	0
							Gaps
							0
QY	276	acctgaactacctggygcccccttcacagacgtgaacttaacatccctcgtgactggyg	335				
DB	26548	AGCTTAAGTACTCTGGGCCCCCTTCAAGAGCCAGACTTCAACCCCTCCCGCTGGGG	26489				
QY	336	cagaacatctgcgccagggccacggtcaacttggaaagtgtgqgaagctcaatgacagc	395				
DB	26488	CAGAACTCTGCCCGAGGGCCACTGTGTGATTGGAGGTGGCGAAGCCCTCAATGACAAAC	26429				
QY	396	tgcgctacaccagagactatgagcggtacagtcacotccctgtgttaactgctgagccca	455				
DB	26428	TTCGGCTGACCCAGAACTACGAGGCTACAGCCACTTCTGTGTACTTGGCTGGCTCA	26369				
QY	456	accgtcagagctgcacacagctgaactcgacgttagccttgccccactctgtacacagctcc	515				
DB	26368	ACCGTCAGGCTCCACTGTGTGAGCTGGCGCCGAGGCTGGCCACATTCTGCACACAGCTCC	26309				
QY	516	agggcctctggygcagcattgcaggtgtcattvgygcagcgtctggtctacaccatctgcccagc	575				
DB	26308	AGGGCTCTGTGGGCGACATTTGGGGCGTCATGTGACGACTCTGGGCTAACCCATCGCCCAAC	26249				
QY	576	ctcttcacagagactagcagcgttggccccctggccccctggccaaagtatctccctccaga	635				
DB	26248	CGCTCCCTGGGACTAACCCACTTGTGACTCCCTGGGCCCTGCCACAGATGACTTCTTCACAA	26189				
QY	636	agatgatgaactctgctgctgctgaagagagctgcagacactgctgctatgagcgttcaagcaag	695				
DB	26188	ACATGAGACACTTTCGGCTGCTGTAAGAGAGCTGCACAGCCTGGCTGTGGGCTCGGCCAAGG	26129				
QY	696	acttcaaccgagcttaagaaagatgacagcctccagcagcttcagtlacacctgtgacttgg	755				
DB	26128	ACTTCAACCGGCTCAAGAAGAGATGACGCTTCACAGCAGCTCACTGCACCTCGACACTGG	26069				
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DB	26068	GGGCTCATGGCTTTCATCTTGCACCTTGCACCTT	26041				

RESULT	10		
LOCUS	AC005849/c		
DEFINITION	AC005849 Homo sapiens chromosome 11 clone CIT-HSP-1337H24, *** SEQUENCING IN PROGRESS ***	169144 bp	HTG 22-OCT-1998
ACCESSION	AC005849		
VERSION	AC005849.1	GI:3779013	
KEYWORDS	HTG; HTGS_PHASE1.		

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
AUTHORS	Smith,D.R.
TITLE	Sequencing of Human Chromosome 10
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 169144)
AUTHORS	Smith,D.R.
TITLE	Direct Submission
JOURNAL	Submitted (22-OCT-1998) Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA 02154, USA
COMMENT	* NOTE: This is a 'working draft' sequence. It currently

```

* consists of 9 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 506: contig of 506 bp in length
*
* 507 3033: contig of 2527 bp in length
*
* 3034 12956: contig of 9923 bp in length
*
* 12957 19521: contig of 6565 bp in length
*
* 19522 31636: contig of 12115 bp in length
*
* 31637 48670: contig of 17034 bp in length
*
* 48671 61610: contig of 12940 bp in length
*
* 61611 97329: contig of 35719 bp in length
*
* 97330 169144: contig of 71815 bp in length
*
* Location/Qualifiers
*
* 1..169144

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
Center project name: H_NH04JG08
----- Project Information -----
Summary Statistics
Sequencing vector: M13; 81%
Sequencing vector: plasmid; 19%
Chemistry: Dye-terminator Big Dye; 22% of reads
Chemistry: Dye-primer ET; 78% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 179377 bases at least Q40
Consensus quality: 177014 bases at least Q30
Consensus quality: 179042 bases at least Q20
Insert size: 179000; agarose-fp
Insert size: 184627; sum-of-contigs
Quality coverage: 5.08 in Q20 bases; agarose-fp
Quality coverage: 5.01 in Q20 bases; sum-of-contigs
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NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1
1126: contig of 1126 bp in length
1127: gap of unknown length
1127: contig of 2172 bp in length
3399: gap of unknown length
3498: gap of unknown length
3499: contig of 2093 bp in length
5592: gap of unknown length
5692: contig of 1648 bp in length
7340: gap of unknown length
7440: contig of 2123 bp in length
9563: gap of unknown length
9663: contig of 2472 bp in length
12135: gap of unknown length
12235: contig of 1839 bp in length
14073: gap of unknown length
14074: gap of unknown length

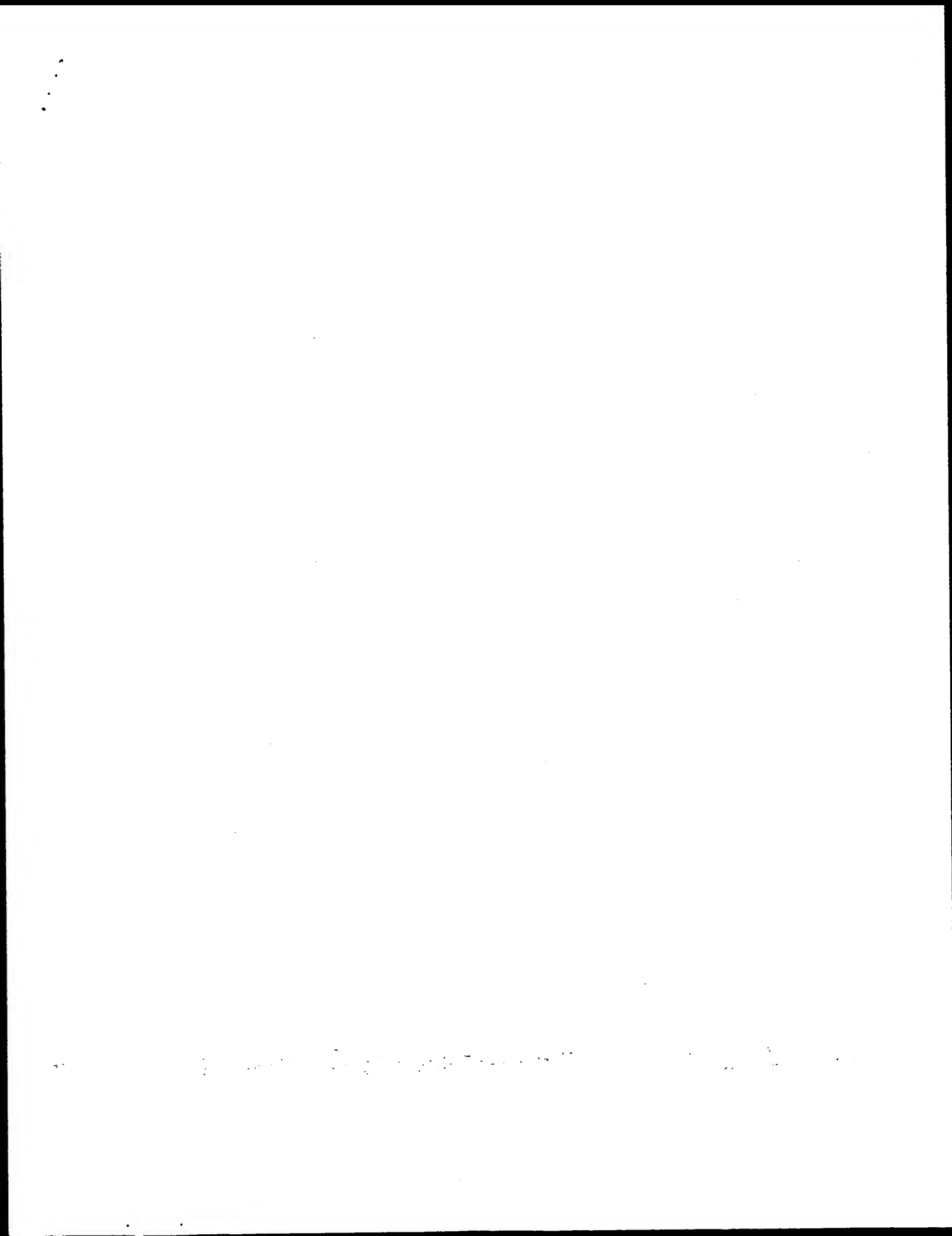
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*	16670	16763	gap of unknown length
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*	22419	22518	gap of unknown length
*	22519	26559	contig of 4041 bp in length
*	26560	26659	gap of unknown length
*	26660	30895	contig of 4236 bp in length
*	30896	30995	gap of unknown length
*	30996	34749	contig of 3754 bp in length
*	34750	34849	gap of unknown length
*	34850	39440	contig of 4591 bp in length
*	39441	39540	gap of unknown length
*	39541	43183	contig of 3643 bp in length
*	43184	43283	gap of unknown length
*	43284	47528	contig of 4245 bp in length
*	47529	47628	gap of unknown length
*	47629	51967	contig of 4339 bp in length
*	51968	52067	gap of unknown length
*	52068	58827	contig of 6760 bp in length
*	58828	58927	gap of unknown length
*	58928	63567	contig of 4640 bp in length
*	63568	63667	gap of unknown length
*	63668	69120	contig of 5453 bp in length
*	69121	69220	gap of unknown length
*	69221	73215	contig of 3995 bp in length
*	73216	73315	gap of unknown length
*	73316	79585	contig of 6270 bp in length
*	79586	79685	gap of unknown length
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*	95857	95956	gap of unknown length
*	95957	102877	contig of 6921 bp in length
*	102878	102977	gap of unknown length
*	102978	110335	contig of 7358 bp in length
*	110336	110435	gap of unknown length
*	110436	120472	contig of 10037 bp in length
*	120473	120573	gap of unknown length
*	120573	132066	contig of 11494 bp in length
*	132067	132166	gap of unknown length
*	132167	144622	contig of 12456 bp in length
*	144623	144722	gap of unknown length
*	144723	156389	contig of 11667 bp in length
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Best Local Similarity 51.3%; Pred.No.1.1;  
Matches 156; Conservative 0; Mismatches 141; Indels 7; Gaps 2;  
  
OY    276  acctgaactactctgtggcccccttccaagcgccctgacctcaatccttcctttctgcctggaggg 335  
DB 103565 AGCTTCACAGTACGAGGGCAGCCCCCTTTAGTGACTCGGTCTTCACCCCTTGAGCTTCACGC 103624  
OY    336  cagaacactctgcccccagggccacgcagctcaactcttgaaagtctgtgcygaagccctcaatgacagagc 395  
DB 103625 TCAGCAGCGCTGCCCTCTCTGCACACGGCTTCTTTAAGACCTGCGCAGCGCCGTGTATGACGGGG 103684  
OY    396  ttgcgcctaacaccagacaatatgagc----gtacagctcaactctctgttaactttgcgttagc 451  
DB 103685 AACGGCTGAGCTTCCACCAGAGGGGCCATTGACCCAGCACTCCACCTCCATTGAGACGAC 103744  
OY    452  c---tcaacccctgcagcctgtcccacagctgaactcgagcctgcagcctgtgccccaatctcylaac 508  
DB 103745 CAGAGCGACTCTAACCCCTGCGACGTGCTCCATCTCTGCGGGCTCAAGCTCGGGGCTCGAGAGACTC 103804
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Mon Mar 18 11:23:40 2002

us-09-931-704-4.rge



GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2002, 09:32:34 ; Search time 1206.01 Seconds

(without alignments)
7297.446 Million cell updates/sec

Title: US-09-931-704-4

Perfect score: 819

Sequence: 1 tatattaaagcttcgcgcg.....agccacagtcagctgtgctt 819

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 11351937 segs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

EST:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	544	66.4	1053	11	BG164929 602343555
2	543	66.3	853	11	BG437538 602489277
3	476	58.1	476	10	BE632644 uv63f01.y
4	464.4	56.7	955	10	AL543945 AL543945
5	333.6	40.7	512	10	AI390475 mu59g08.y
6	312.4	38.1	407	10	AI752561 mu59g08.y
7	261.2	31.9	488	10	AA015243 mu59g08.y
8	246.8	30.1	552	11	AA015243 mu59g08.y
9	228.4	27.9	440	11	BG095271 mu59g07.x
10	172.8	21.1	915	11	BG148676 mu59g07.y
11	124.8	15.2	691	11	BF035982 mu59g07.y
12	66.4	8.1	180	10	AA204015 mu59g08.r

13	50.8	6.2	711	11	BG758365
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15	45	5.5	925	13	CNS0091P
16	43.4	5.3	936	13	CNS01SR2
17	43.4	5.3	1101	13	CNS01258
18	42.8	5.2	844	13	CNS0052P
19	42.8	5.2	932	13	CNS00720
20	42.4	5.2	505	10	AI984845
21	42.4	5.2	658	10	AW873554
22	42.4	5.2	690	11	BF732971
23	42.4	5.2	787	11	BF971932
24	42.4	5.2	983	11	BF327781
25	42	5.1	839	13	CNS004NB
26	41.6	5.1	511	10	BE754133
27	41	5.0	342	11	BI345660
28	41	5.0	778	13	AO327192
29	41	5.0	1203	13	CNS015V4
30	40.8	5.0	525	11	BE808147
31	40.8	5.0	603	10	AI039288
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34	40.4	4.9	268	10	AW355114
35	40.4	4.9	776	13	CNS010RY
36	40.2	4.9	797	13	CNS04NGE
37	40.2	4.9	828	13	CNS04GHZ
38	40	4.9	935	13	CNS006XK
39	39.6	4.8	586	10	AV670279
40	39.4	4.8	467	10	AW657443
41	39.4	4.8	529	10	BE033291
42	39.4	4.8	978	10	BE614877
43	39.4	4.8	1009	13	CNS010EW
44	39	4.8	1281	11	BG852363
45	38.8	4.7	995	10	AL538217

ALIGNMENTS

RESULT 1

LOCUS BG164929 1053 bp mRNA EST

DEFINITION 602343555F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:4453813 5', mRNA sequence.

ACCESSION BG164929

VERSION BG164929.1 GI:12671563

KEYWORDS EST.

SOURCE Human.

ORGANISM Homo sapiens

REFERENCE NIH-MGC <http://mgc.nhl.nih.gov/>.

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@pds-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: L1AM10244 row: m column: 14

High quality sequence start: 675.

High quality sequence stop: 675.

Location/Qualifiers

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/db_xref="taxon:9606"

/clone="IMAGE:4453813"

/clone_lib="NIH_MGC_89"

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QY	713	aagaagaatgcagcctcccaag - cagcttcagctcaacc - - - tgcactctggagcacaatgatt	768
Db	659	aagaagaatgcagcctcccaagcctccagcactgcagtaaccatgcacacttggaagggctcatagggatt	718
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DEFINITION	BE632644	476 bp	mRNA	EST
ACCESSION	U63101.1	Soares mouse	3MDMS	Mus musculus cdna clone IMAGE:3411865
VERSION	5,	mRNA sequence.		
KEYWORDS	BE632644			
SOURCE	BE632644.1	GI:915332		
ORGANISM	EST.			
	house mouse.			
	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Mus.			
TITLE	1 (bases 1 to 476)			
	NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap .			
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),			
JOURNAL	Tumor Gene Index			
COMMENT	Unpublished (1997)			
	Contact: Robert Strausberg, Ph.D.			
	Email: cgapds@remail.nih.gov			
	This clone is available royalty-free through LNL; contact the			
	IMAGE Consortium (info@image.llnl.gov) for further information.			
	MC1:1087877			
	Seq primer: -40RP from GIBCO			
	High quality sequence stop: 464.			

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was primed with a Not I - oligo(47) primer [5',
TGTACCAATCATCTAGAGTGCGAGCGCGCCGCTGTATTTTATTTTATTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT73 vector. RNA
provided by Dr. Bertrand Jordan. Library went through
three rounds of normalization, and was constructed by
Bento Soares and M.Fatima Bonaldo."
93 a 165 c 126 g 92 t

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Query Match      58.1%; Score 476; DB 10; Length 476;
Best Local Similarity 100.0%; Pred. No. 1e-94;
Matches 476; Conservative 0; Mismatches 0; Indel.; 0; Gaps 0;

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QY	323	cctgcgactggggcaggaanaactctgcgccagggccacaggtcaacttggaaagtgtaggaagc	382
Db	121	CCTGCAGCTGGGGCAGAAACTCTGCCCCAGGCGACAGGTCAACTTGGAAATGGGGGAAGC	180
QY	383	ctcaatgaaggcgtcgcgctgtgacccagaactatgaagcgtagacagccctcctgtgttac	442
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VERSION	AL543945.1	GI:12876424	
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ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Li W.B., Gruber C., Jessee J. and Polayes D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
CONTACT	Genoscope - Centre National de Sequencage		
FEATURES	Genoscope - Centre National de Sequencage		
SOURCE	BP 191 91006 EVRY cedex - France		
	Email: seque@genoscope.cns.fr, web : www.genoscope.cns.fr.		
	Location/Qualifiers		
	I. .955		

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/db_xref="taxon:9606"
/clone="CSOD1004YM15"
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/tissue_type="placenta"
/notes="Vector: pCMVSport 6; Site 1: NotI; 1st strand cDNA
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSport 6
vector. Library was normalized. Library was constructed by
life technologies. Contact : Feng Liang life technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371

```


LOCUS	AI752561	407 bp	mRNA	EST	22-JUN-1999
DEFINITION	cn17d05.x1.Norm1 Human Trabecular Bone Cells Homo sapiens CDNA				
ACCESSION	AI752561				
VERSION	AI752561.1	GI:5130825			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 407) Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M., Robey				
TITLE	SGAP: The Skeletal Genome Anatomy Project				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Libin Jia National Human Genome Research Institute 10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA Tel: 301-402-4877 Fax: 301-496-7157 Email: libin@nih.gov DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC). Plate: 17 row: d column: 05 Seq primer: -21M13 forward primer (ABI). Location/Qualifiers 1..407 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="NHBC-cn17d05" /clone_lib="Normal Human Trabecular Bone Cells" /sex="Female" /issue_type="Bone" /cell_type="Trabecular Bone Cells" /lab_host="SURE" /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI"				
FEATURES	source				
BASE COUNT	68 a 148 c 110 g 81 t				
ORIGIN					
Query Match	38.1%; Score 312.4; DB 10; Length 407;				
Best Local Similarity	90.3%; Pred. No. 8.1e-59;				
Matches 334; Conservative	0; Mismatches 36; Indels 0; Gaps 0;				
414	atgaagcgtaagctactctctgttcttcttgctgctgagctcaacgctcaagctgcacag	473			
9	acgaagccctacagccacacctctgtgttactgctgagcctcaacgctgcacagc	68			
474	ctgaactccgaagttagctctgagccacctctgtgacagcctcaaggccctgagca	533			
69	ctgacctgctggccggcagcctgagccaccttctgacacagcctccaggccctgctggcagca	128			
534	ttgcagtgatcattgagcagcgtctggtctaccacatgcccagcctctgcccaggaactgagc	593			
129	ttgctggggctatgacacctctggcctgacccacctgcccagccgctgctggagctgaac	188			
594	cagcttgagccctctgctgctgcccacagtgactctctccagaagatgatatctctgac	653			
189	ccacttggactcttgccctgcccacagtgactctctccagaagatgatatctctgac	248			
654	tgctaaagagctgagacacctgtatgagcgttcaagccagaagactcaacagcgttaaga	713			
249	tgctaaagagctgagacacctgtatgagcgttcaagccagaagactcaacagcgttaaga	308			
714	agaagatgagcctccagcagcttcaagcacttcaagcacttggaggtacatggtttctgac	773			
309	agaagatgagcctccagcagcttcaagcacttcaagcacttggaggtacatggtttctgac	368			
774	ctctgacct 783				
369	ttctgacct 378				

[illegible]

Db	175	GAGGATGTAGTTCGCTATGACACGGAGTGTGTGGCA - CTCCTGACAACTGGCAGGCTTTAA	233
Qy	182	cgcaaaagagatccaaagcgccctgccccctccatccagaataactatagactcaaccgctac	241
Db	234	CGCACAGGAGATCCAGGCGCCCTGCGCCCTCCATCCACGAAAAACCTATGACTCCACCGCTAC	293
Qy	242	ctgagacatcaactccagactagctgtggaactact	279
Db	294	CTGGAGCATCAACTCCGACGCTTACTGTGGAGCACTACGT	331
RESULT	8		
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DEFINITION	BC095271	552 bp	EST
ACCESSION	U859407.x1	Soares mouse NMGB.bcell Mus musculus cDNA clone	26-JAN-2001
VERSION	IMAGE:3383604	3', similar to TF:Q9QZM3 Q9QZM3 NEUROTROPHIN-1/B-CELL	
KEYWORDS	STIMULATING FACTOR-3	''	mRNA sequence.
SOURCE	BC095271.1	GI:12577834	
ORGANISM	EST.		
REFERENCE	house mouse.		
AUTHORS	Mus musculus		
TITLE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
JOURNAL	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
COMMENT	NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	This clone is available royalty-free through LBNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MGJ:1088600		
FEATURES	High quality sequence stop: 444.		
SOURCE	location/Qualifiers		
	1..552		
	/organism="Mus musculus"		
	/db_xref="taxon:10090"		
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	/clone_lib="Soares mouse NMGB.bcell"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: germinal B-cell; Vector: pRT73D-Pac		
	(pharmacia) with a modified polylinker; Site_1: Not I;		
	Site_2: Eco RI; 1st strand cDNA was primed with a Not I -		
	oligo(dT) primer [5',		
	TGTTACCAATCTGAAGTGGAGCGCGCCGCTGTTTTTTTTTTTTTTTTTTTTTTTTTT		
	T 3']; double-stranded cDNA was ligated to Eco RI		
	adaptors (Pharmacia), digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pRT73 vector.		
	Library is normalized; constructed by Bento Soares and		
	M.Patrina Bonaldo."		
BASE COUNT	147 a 125 c 147 g 131 t	2 others	
ORIGIN			
Query Match	30.1%; Score 246.8; DB 11; Length 552;		
Best Local Similarity	96.3%; Pred. No. 2.1e-44;		
Matches	262; Conservative 0; Mismatches 9; Indels 1; Gaps 1;		
Qy	548	gagacgttgctaccacacgctccagacctctgcagaagactgaacagcctgggccccct	607
Db	552	GCGATGCTTGCTGCTACCCACTGCTGCTTTGGCAGGAGCTGACCGCTGGGCGCCCT	493
Qy	608	ggccctggcccaagagactctccagaagatgagatgctctgtgctctggaagagctg	667
Db	492	GGCCCTGCCCCACAGAGCATCTCCACGAAGAAGATGATGACTTCTGGCTG-TTAAAGAGCTG	434
Qy	668	cagaactgtcatgcygtctcagcaagaagactcaaccgctctaaagaagaatgtcaagcct	727
Db	433	CAGACCTGCGTATGGCGTTACAGCCAAAGACATTCACACCGGCTTAAAGAAGAATGACAGCT	374
Qy	728	ccaagcagcttcaagtaacctgcgaacttggaagacaatggtttcttgaccttgacccttaac	787

DB	373	CCAGCAGCTTCAAGTACACCTGCACCTTGGAGGCCCATGTTTGTGACCTTTGACCTTAAC	314
OY	788	ccccacacctcagagccagtcagctgtgctt	819
Db	313	CCCCACACCTCCAGGCCCGCAGTCAGCTGTCTT	282
RESULT	9		
LOCUS	BG148676		
DEFINITION	BG148676	440 bp	mRNA
ACCESSION	u855g07.y1	Soares_mouse_MNGB_bcell	Mus musculus cDNA clone
VERSION	IMAGE:3383604.5	similar to	FR:Q9QZM3.Q9QZM3 NEUROPROPHIN-1/B-CELL
KEYWORDS	STIMULATING FACTOR-3	;	mRNA sequence.
ORGANISM	BG148676	GI:12652098	
SOURCE	EST.		
REFERENCE	house mouse.		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
JOURNAL	NCI-CCAP	http://www.ncbi.nlm.nih.gov/ncicgap.	
COMMENT	unpublished (1997)		
	Other ESTs: u855g07.x1		
	Contact: Robert Strausberg, Ph.D.		
	Email: cga@bbs-remail.nih.gov		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Seq primer: -40RP from gibco		
	MG:1088600		
FEATURES	High quality sequence stop: 431.		
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	/clone="IMAGE:3383604"		
	/clone_lib="Soares_mouse_MNGB_bcell"		
	/lab_host="DH10B (phage-resistant)"		
	/note="Organ: germinal B-cell; Vector: p130-Pac		
	/phenotype="A cell with a modified polylinker; Site: 1; Not I:		
	Site-2; Eco RI: 1st strand cDNA was primed with a Not I -		
	oligo(dT) primer (5'		
	TGTACCAATCTGAAGTGGAGGAGCGGCCCTGTGTTTTTTTTTTTTTTTTTT		
	T 3']; double-stranded cDNA was ligated to Eco RI		
	adaptors (Pharmacia); digested with Not I and cloned into		
	the Not I and Eco RI sites of the modified pRT3 vector.		
	Library is normalized; constructed by Benito Soares and		
	M.Felina Bonaide."		
BASE COUNT	99 a	127 c	106 t
ORIGIN			
Query Match	27.9%;	Score 228.4;	DB 11; Length 440;
Best Local Similarity	99.6%;	Pred. No. 2.3e-40;	
Matches	229;	Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	590	gagcagccttgagcccttgagcccttgagccagtgagcttcttcagagaatggaugacttc	649
Db	1	GAGCCAGCCTGGGCCCCCTGGCCCTCCCAACAGTAGCTCTCCAGAGATGATGACTTC	60
OY	650	tggctgtcgaagaagactcacagaccttggtctatggttggttaagccaagaagactcaacggctt	709
Db	61	TGGCTGCTGAAGAGAGACTGCAGACTGGGCTATGGGCTTTCAGCCAAAGACTTCACAGGGCTT	120
OY	710	aagaagaagatgcagccttcacagcagcttcacgtacccttcgacacttggaagacaatggtcttc	769
Db	121	AAGAAGAGATGCACGCTCCAGCAGCTTCAGTCACCTCGACCTTGGAGGCCCATGCTTC	180
OY	770	tgaacctgaccccttaacccccacaccttcacagagccagctcagctgtgctt	819

PR 30-JAN-1998: 980S-0016534.
 PR 03-FEB-1997: 97US-0792019.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Chang M, Elliot GS, Sarmiento U, Senaldi G;
 DR WPI: 1998-437475/37.
 DR P-PSDB: AAM29716.
 XX
 XX Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 PT immunological diseases or inflammation, also as vaccine adjuvant
 XX
 XX Disclosure: Fig 4; 120pp; English.
 XX
 XX This newly isolated mouse cDNA sequence codes for a novel
 CC neurotrophic factor, designated NNT-1 (see AAM29716), that is a
 CC growth factor for neurons and for B or T cells. Vectors and
 CC host cells are provided for use in the production of murine and
 CC human NNT-1 polypeptides. These are used to treat: (i) neurological
 CC or immunological diseases, specifically Alzheimer's, Parkinson's or
 CC Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective IgA deficiency, hypogammaglobulinaemia and X-linked
 CC agammaglobulinaemia (claimed), but many others disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. NNT-1 nucleic acid fragments are also used as
 CC hybridisation probes in diagnostic assays. In addition, cells that
 CC have been engineered to express NNT-1 can be implanted, or nucleic
 CC acids are delivered in gene therapy vectors.
 XX
 XX Sequence 819 BP; 156 A; 288 C; 218 G; 157 T; 0 other;
 XX
 Query Match 100.0%; Score 819; DB 19; Length 819;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 819; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 421 gtaacgtcaactctctgttacttgcgtggtcctcaaccgctcaagctctgctcaact 480
 QY 481 ccgacgtacacttggccactctctgtaccagctcccaaggctctggcagcatgtcag 540
 DB 481 ccgacgtacacttggccactctctgtaccagctcccaaggctctggcagcatgtcag 540
 QY 541 tctcagcagcacttgcctacacttgcctccagcctctgcagagcactgagcctc 600
 DB 541 tctcagcagcacttgcctacacttgcctccagcctctgcagagcactgagcctc 600
 QY 601 ggcctctggcctctgcctccagcagtgactctccctccagaaatgatactctgtc 660
 DB 601 ggcctctggcctctgcctccagcagtgactctccctccagaaatgatactctgtc 660
 QY 661 ggcctctggcctctgcctccagcagtgactctccctccagaaatgatactctgtc 720
 DB 661 ggcctctggcctctgcctccagcagtgactctccctccagaaatgatactctgtc 720
 QY 721 gcaagctcagcagctcagctcagctcagctcagctcagctcagctcagctcag 780
 DB 721 gcaagctcagcagctcagctcagctcagctcagctcagctcagctcagctcag 780
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 DB 781 ccttaaccccaacactccagcagcagcagcagcagcagcagcagcagcagcagc 819

RESULT 2
 AAV22654
 ID AAV22654 standard; cDNA; 819 BP.
 XX
 XX AAV22654;
 AC
 AC 13-JUL-1998 (first entry)
 DT
 DT
 XX
 XX cDNA encoding murine neurotrophic factor NNT-1.
 DE
 XX
 XX Mouse: neurotrophic factor; NNT-1; growth; motor; synu; atic; neuron;
 KW treatment; neurological disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimers's disease; stroke; ss.
 XX
 XX Mus sp.
 XX
 XX US5741772-A.
 XX 21-APR-1998.
 XX
 XX 03-FEB-1997; 97US-0792019.
 XX
 XX 03-FEB-1997; 97US-0792019.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M;
 XX
 XX WPI: 1998-260526/23.
 XX P-PSDB: AAM56142.
 XX
 XX Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
 PT useful for stimulating growth of motor and sympathetic neurons
 XX
 XX Disclosure: Fig 4; 41pp; English.
 XX
 XX The present sequence encodes a murine neurotrophic factor, designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic


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Db      261  cgcacagggagccagggccttgccctccatccagaaacatgatgacctaccgcgtac
QY      242  ctggagcatcaactcgcagacttagctggagactactgaactactgggcccccttc
Db      321  ctggagcatcaactcgcagacttagctggagactactgaactactgggcccccttc
QY      302  aacagagctgactcaactctctcgcactgagggagagcaaacctctgcccagggccagctc
Db      381  aacagagctgactcaactctctcgcactgagggagagcaaacctctgcccagggccagctc
QY      362  aacttgagagtggtgcgaagctcaatgacagagctgcggtctgacccagaactatgagcg
Db      441  gacttgagagtggtgcgaagctcaatgacagagctgcggtctgacccagaactatgagcg
QY      422  tacagtcacctcctgttacttgctggtggtcctaacgctgaagctggtccagagctgaatc
Db      501  tacagtcacctcctgttacttgctggtggtcctaacgctgaagctggtccagagctgaatc
QY      482  cgaagtcagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
Db      561  cgcgcagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
QY      542  gtcacgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
Db      621  gtcacgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
QY      602  gtcacgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
Db      681  actctgtgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
QY      662  gagctgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
Db      741  gagctgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
QY      722  gagctgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
Db      801  gagctgagagctggtcgtcgtctgtacagagctcagaggtcgtctggtgagagctgaggt
QY      782  ct 783
Db      861  tt 862

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RESULT 5
AAA88546
ID AAA88546 standard; DNA; 1790 BP.
XX
AC AAA88546;
XX
XX 22-JAN-2001 (first entry)
XX
XX Human Interleukin-B60 (IL-B60) gene.
XX
XX Interleukin-B60; IL-B60; human; cytokine; chromosome 11;
XX cytokine-like factor-1; haematopoietic; inflammation;
XX antiinflammatory; autoimmune disease; therapy; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 162..809
XX FT /*tag= a
XX FT sig_peptide 162..212
XX FT /*tag= b
XX FT mat_peptide 213..806
XX FT /*tag= c
XX
XX WO200053631-A1.
XX
XX 14-SEP-2000.
XX
XX 09-MAR-2000; 2000MO-US06182.
XX

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PR      11-MAR-1999; 99US-0267901.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Opmann B, Timans JC, Kastelein RA, Bazan JF;
XX
XX WPI: 2000-587426/55.
XX
XX P-PSDB: AAB19686.
XX
XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
XX polypeptides, and nucleic acids, useful in research, diagnosis and for
XX treating inflammatory and autoimmune disorders.
XX
XX Claim 17; Page 15-16; 97pp; English.
XX
XX The present sequence is that of DNA encoding human interleukin-B60
XX (IL-B60, see AAB19586), a novel, small soluble cytokine-like protein
XX of 198 amino acids that exhibits structural motifs characteristic
XX of a member of the long-chain cytokines, and which shows homology
XX to granulocyte colony stimulating factor and interleukin 6. IL-60B
XX may have either stimulatory or inhibitory effects on haematopoietic
XX cells, including e.g. lymphoid cells, such as T-cells, B-cells,
XX natural killer cells, macrophages, dendritic cells, haematopoietic
XX progenitors, etc. Methods are provided for modulating the
XX physiology or development of a cell or tissue culture cells by
XX contacting the cell with an agonist or antagonist of IL-B60 or an
XX agonist of antagonist of a complex of mature IL-B60 and its
XX partner, cytokine-like factor-1 (CLF-1, see AAB19586). The
XX IL-B60/CLF-1 cytokine serves as a key physiological factor in motor
XX neuron development and regeneration. IL-60B, its agonists and
XX antagonists may be used to treat inflammatory or autoimmune
XX disorders and also for drug screening. The IL60B gene maps to
XX human chromosome 11.
XX
XX Sequence 1790 BP; 381 A; 560 C; 474 G; 375 T; 0 other:
XX
XX Query Match 82.3%; Score 674; DB 21; Length 1790;
XX Best Local Similarity 92.2%; Pred. No. 6,6e-160;
XX Matches 721; Conservative 0; Mismatches 60; Indels 1; Gaps 1;

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QY      62  gagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 121
Db      100  gagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 158
QY      122  gggatgttagcttgctcgtacagcgtgctgtgacacgtccctccctcgcagcgcgcgcgc 181
Db      159  gggatgttagcgtgctcgtacagcgtgctgtgacacgtccctccctcgcagcgcgcgcgc 218
QY      182  cgcacagagatccagagcctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 241
Db      219  cgcacagagagcagagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 278
QY      242  ctggagcatcaactcgcagacttagctggagagctgaactgaactcctggtggtccttc 301
Db      279  ctggagcatcaactcgcagacttagctggagagctgaactgaactcctggtggtccttc 338
QY      302  aacagagctgactcaactctcctcgcactgaggggagagaaactcgtccgcgcgcgcgcgc 361
Db      339  aacagagagactcaactcctcctcgcactgaggggagagaaactcgtccgcgcgcgcgcgc 398
QY      362  aacttgagagtggtgcgaagctcaatgacagagctgcggtctgacccagaactatgagcg 421
Db      399  gacttgagagtggtgcgaagctcaatgacagagctgcggtctgacccagaactatgagcg 458
QY      422  tacagtcacctcctgttacttgctggtggtcctaacgctgaagctggtcgcacacctggaac 481
Db      459  tacagtcacctcctgttacttgctggtggtcctaacgctgaagctggtcgcacacctggaac 518

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QY	482	cgacgtacgtcgccacattctgtacacagctccaaggccgtctggagacattgtcagat	545
Db	519	cgccgacacgtggcccaattctgtacacagacctccaaggccctgtgcgagattgtcggc	578
QY	542	gtacatgctgacgctgtgtgtacccaactgccacagcctctgcacagagattggccaagccttg	601
Db	579	gtacatgacagctctgtgtgtacccaactgccacagcctctgtgcagattggccaacacttg	638
QY	602	ggcccttgcccttgcacacagagattctctccaagaagtgtgactctgtgcgtgtgaag	661
Db	639	actctctgaccttgcaccaagaatgtacctctccaagaagaatgtacactctgtgcgtgaag	698
QY	662	gagctgtcagacactgtgtctatgtgcgtcttcacgccaagaagattccaacggctcttaagaagaagt	721
Db	699	gagctgtcagacactgtgtctgtgcgtctgcgccaagaagattccaacggctcttaagaagaagt	758
QY	722	cagctctcagacagcttcaatcacaccctgtcatttgagacatagtcttcagacctgacc	781
Db	759	cagctctcagacagcttcaatcacaccctgtcatttgagacatagtcttcagacctgacc	818
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Db	819	tt 820	

RESULT	6
AAV47510	
ID	AAV47510 standard; cDNA; 797 BP.
XX	

AC AAV47510;
XY

09-NOV-1998 (first entry)

Human neurotrophic factor NNT-1 cDNA

KW NMI-1; neurotrophic factor; human; antiinflammatory; adjuvant;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW peripheral neuropathy; dystrophy; neural retina degeneration;
KW common variable immunodeficiency; CVID; selective IgA deficiency;
KW hypogammaglobulinemia; X-linked agammaglobulinaemia; antiseptic,
therapy; ss

Homo sapiens.

Location/Qualifiers
90 7657

sig_peptide

mat_peptide	171..764
FT	

1- 220220001
XX
XX

06 - AUG - 1998

02-FEB-1998

30-JAN-1998

XX

Chandra M. El Jai et al.

WPI: 1998-43

✕

factor NNT-1

X

1

Claim 3; Fig 1; 120pp; English
ps
xy

CC codes of a novel neurotrophic factor, designated as NT-1 (88295)
CC AN29715), that is a growth factor for neurons and is secreted by T cells
CC It was obtained from a T-cell lymphoma cDNA library by cDNA screening
CC sequence tag analysis on the basis of homology to CNTF. The
CC isolated NT-1 cDNA was used as probe to isolated NT-1 genomic
CC DNA (see AAV47511). Vectors containing the cDNA or genomic DNA and
CC host cells are provided for use in the production of NT-1
CC polypeptides. These are used to treat: (i) neurological or
CC immunological diseases, specifically Alzheimer's, Parkinson's or
CC Huntington's diseases, amyotrophic lateral sclerosis,
CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
CC degeneration of the neural retina, or conditions characterized by T
CC or B cell defects, e.g. common variable immunodeficiency (CVID),
CC selective IgA deficiency, hypogammaglobulinemia and X-linked
CC agammaglobulinemia (claimed), but many others disclosed, and (ii)
CC inflammation. NT-1 is also able to boost immunoreactivity and
CC antibody production following vaccination, and, since it inhibits
CC tumour necrosis factor production, it may also be useful for
CC treating sepsis. NT-1 nucleic acid fragments are also used as
CC hybridisation probes in diagnostic assays. In addition, cells that
CC have been engineered to express NT-1 can be implanted, or nucleic
CC acids are delivered in gene therapy vectors.

sequence / 51 BF; 139 A; 29 / C; 218 G; 143 T; 0 other

Query Match	81.7%	Score 669.4	DB 19	Length 797
-------------	-------	-------------	-------	------------

Matches 717; Conservative 0; Mismatches 61;

1

[illegible]

KW	NNT-1; human; neurotrophic factor; nootropic; neuropathic; live; treatment;
KW	anticonvulsant; antiParkinsonian; antidiabetic; ophthalmological;
KW	neurosy system degeneration; Alzheimer's disease; Parkinson's disease;
KW	amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW	Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW	retinopathy; immune disorder; hematopoietic disorder; ss.
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OS	Homo sapiens.
XX	
FI	
FT	
key	Location/Qualifiers
CDS	90..767
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FT      /tag= 9
FT      /number= 2
FT      3366..3857
FT      /tag= h
FT      /number= 3
PN      WO9833922-A1.
XX      06-AUG-1998.
XX      02-FEB-1998: 98WO-US02363.
XX      30-JAN-1998: 98US-0016534.
XX      03-FEB-1997: 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M, Elliot GS, Sarmiento U, Senaldi G;
XX      WPI: 1998-437475/37.
XX      P-PSDB: AAW29715.
XX      Newly isolated nucleic acid encoding human or murine neurotrophic
XX      factor NNT-1 - useful for treatment of neurological and
XX      immunological diseases or inflammation, also as vaccine adjuvant
XX      Claim 4; Fig 2; 120pp; English.
XX      This newly isolated human genomic DNA sequence (deposited at
XX      ATCC 98294) codes for a novel neurotrophic factor, designated NNT-1
XX      (see AAW29715), that is a growth factor for neurons and for B or T
XX      cells. It was obtained from a human genomic P1 library using the
XX      human NNT-1 cDNA (see AAW47510) as probe. Vectors containing the
XX      cDNA or genomic DNA and host cells are provided for use in the
XX      production of NNT-1 polypeptides. These are used to treat: (1)
XX      neurological or immunological diseases, specifically Alzheimer's,
XX      Parkinson's or Huntington's diseases, amyotrophic lateral sclerosis,
XX      Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
XX      degeneration of the neural retina, or conditions characterized by T
XX      or B cell defects, e.g. common variable immunodeficiency (CVID),
XX      selective IGA deficiency, hypogammaglobulinemia and X-linked
XX      agammaglobulinemia (claimed), but many others disclosed; and (11)
XX      inflammation. NNT-1 is also able to boost immunoreactivity and
XX      antibody production following vaccination, and since it inhibits
XX      tumour necrosis factor production, it may also be useful for
XX      treating sepsis. NNT-1 nucleic acid fragments are also used as
XX      hybridisation probes in diagnostic assays. In addition, cells that
XX      have been engineered to express NNT-1 can be implanted, or nucleic
XX      acids are delivered in gene therapy vectors.
XX      Sequence 5088 BP; 992 A; 1746 C; 1191 G; 1158 T; 1 other:
SQ

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Query Match      52.5%; Score 429.6; DB 19; Length 5088;
Best Local Similarity 90.4%; Pred. No. 1.9e-98;
Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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QY      576 cctctgagcagcctgagcagccttggccctggccttgccacagatgacttctccaga 635
DB      3664 cctctgagcagccttgcagcagccttggccctggccttgccacagatgacttctccaga 3723
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QY      756 aggcacatggttctgaccttgacct 783
DB      3844 gggcctatggttctgaccttgacct 3871

RESULT 15
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ID      AAV22653 standard; DNA: 5088 BP.
XX      AAV22653:
XX      13-JUL-1998 (first entry)
XX      Human genomic DNA encoding neurotrophic factor NNT-1.
XX      Human: neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
XX      treatment; neurological disease; degeneration; Parkinson's disease;
XX      amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke; ss.
XX      Homo sapiens.
XX      OS
XX      Key Location/Qualifiers
XX      FT 138 /*tag= a
XX      FT misc-feature /*note= "represents intervening unsequenced region
XX      of 1 Kb"
XX      FT 138
XX      US5741772-A.
XX      21-APR-1998.
XX      03-FEB-1997: 97US-0792019.
XX      03-FEB-1997: 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M;
XX      WPI: 1998-260526/23.
XX      Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
XX      useful for stimulating growth of motor and sympathetic neurons
XX      Disclosure; Fig 2; 41pp; English.
XX      The present sequence encodes a human neurotrophic factor designated
XX      NNT-1, which is capable of stimulating growth of motor and sympathetic
XX      neurons. The NNT-1 protein is useful in the treatment of neurological
XX      diseases characterised by the degeneration and death of particular
XX      classes of neurons. These diseases specifically include Parkinson's
XX      disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
XX      stroke and various degenerative disorders affecting vision.
XX      Sequence 5088 BP; 992 A; 1746 C; 1191 G; 1158 T; 1 other:
SQ

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2002, 09:37:40 ; Search time 44.41 Seconds
(without alignments)
4176.660 Million cell updates/sec

Title: US-09-931-704-4
Perfect score: 819
Sequence: 1 tatataaagcttcgccg.....agcccaagtcagctgtcctt 819

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
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2: /cgn2_6/ptodata/2/ina/5B.COMB.seq: *
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_6/ptodata/2/ina/PCBUS.COMB.seq: *
6: /cgn2_6/ptodata/2/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	819	100.0	819	1	US-08-792-019B-4 Sequence 4, Appli
2	819	100.0	819	3	US-08-988-819-4 Sequence 4, Appli
3	819	100.0	819	3	US-09-016-534-4 Sequence 4, Appli
4	669.4	81.7	797	1	US-08-792-019B-1 Sequence 1, Appli
5	669.4	81.7	797	3	US-08-988-819-1 Sequence 1, Appli
6	669.4	81.7	797	3	US-09-016-534-1 Sequence 1, Appli
7	627	76.6	1710	3	US-09-106-182-1 Sequence 1, Appli
8	429.6	52.5	5087	3	US-08-792-019B-3 Sequence 3, Appli
9	429.6	52.5	5087	3	US-08-988-819-3 Sequence 3, Appli
10	429.6	52.5	5087	3	US-09-016-534-3 Sequence 3, Appli
11	52	6.3	396	3	US-09-106-182-7 Sequence 1, Appli
12	43.2	5.3	6803	3	US-08-665-259-19 Sequence 19, Appli
13	43.2	5.3	6803	3	US-08-762-500-19 Sequence 19, Appli
14	42.4	5.2	1642	2	US-08-665-037-1 Sequence 1, Appli
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18	34.8	4.2	4403765	4	US-09-103-840A-2 Sequence 2, Appli
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21	34.4	4.2	1225	1	US-08-275-370-1 Sequence 1, Appli
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23	33.6	4.1	36519	3	US-08-923-137-2 Sequence 2, Appli
24	33.4	4.1	1117	4	US-09-347-819-5 Sequence 5, Appli
25	33.2	4.1	1600	3	US-08-602-791-1 Sequence 1, Appli
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C 36	32	3.9	856	3	US-09-188-930-16	Sequence 16, Appli
C 37	32	3.9	5337	2	US-08-784-512-4	Sequence 4, Appli
C 38	32	3.9	5337	2	US-09-176-228-4	Sequence 2, Appli
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C 40	31.8	3.9	2881	1	US-08-396-479B-5	Sequence 5, Appli
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C 42	31.8	3.9	3226	3	US-08-870-126-10	Sequence 10, Appli
C 43	31.6	3.9	745	1	US-08-036-555B-163	Sequence 163, App
C 44	31.6	3.9	745	1	US-08-469-559-163	Sequence 163, App
C 45	31.6	3.9	745	1	US-08-249-322A-163	Sequence 163, App

ALIGNMENTS

RESULT 1
US-08-792-019B-4
; Sequence 4, Application US/08792019B
; Patent No. 5741772
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: AMGEN INC.
; STREET: 1840 DEHAVILLAND DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,019B
; FILING DATE: 03-FEB-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 819 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 95..769
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: 176..769
; FEATURE:
; NAME/KEY: sig-peptide
; LOCATION: 95..175
; US-08-792-019B-4
Query Match 100.0%; Score 819; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. NO. 6e-206;
Matches 819; Conservative 0; Mismatches 0; Gaps 0;

[illegible]

RESULT 2
US-08-968-819-4
Sequence 4, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

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? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/988,819
? FILING DATE: 12-DEC-1997
? CLASSIFICATION: 536
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/792,019
? FILING DATE: 03-FEB-1997
? ATTORNEY/AGENT INFORMATION:
? NAME: COOK, ROBERT R.
? REGISTRATION NUMBER: 31,602
? REFERENCE/DOCKET NUMBER: A-442A
? INFORMATION FOR SEQ ID NO: 4:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 819 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 95..769
? FEATURE:
? NAME/KEY: mat_peptide
? LOCATION: 176..769
? FEATURE:
? NAME/KEY: sig_peptide
? LOCATION: 95..175
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? US-08-988-819-4

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1 ADDRESS: AMGEN INC.
2 STREET: 1840 DEHAVILLAND DRIVE
3 CITY: THOUSAND OAKS
4 STATE: CA
5 COUNTRY: USA
6 ZIP: 91320
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: Floppy disk
9 COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/792,019B
14 FILING DATE: 03-FEB-1997
15 CLASSIFICATION: 514
16 ATTORNEY/AGENT INFORMATION:
17 NAME: COOK, ROBERT R.
18 REGISTRATION NUMBER: 31,602
19 REFERENCE/DOCKET NUMBER: A-442
20 INFORMATION FOR SEQ ID NO: 1:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 797 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
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27 FEATURE:
28 NAME/KEY: CDS
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36 US-08-792-0199-1

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[illegible]

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QY	545	atggcgaagcttggctlaaccacatgccccagcctctgcgcagagctgagctgagctgagctgagc	604
Db	540	ATGGCAGACTGTGGGCTGTACCCACTGTGCCCGCCAGCGGCTGCTGGGAGCTGAMCCCACTTGGACT	599
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	; Sequence 1, Application us/08988819		
	; Patent No. 6054294		
	GENERAL INFORMATION:		
	APPLICANT: CHANG, MING-SHI		
	TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1		
	NUMBER OF SEQUENCES: 16		
	CORRESPONDENCE ADDRESS:		
	ADDRESSEE: AMGEN INC.		
	STREET: ONE AMGEN CENTER DRIVE		
	CITY: THOUSAND OAKS		
	STATE: CA		
	COUNTRY: USA		
	ZIP: 91320		
	COMPUTER READABLE FORM:		
	MEDIUM TYPE: Floppy disk		
	COMPUTER: IBM PC compatible		
	OPERATING SYSTEM: PC-DOS/MS-DOS		
	SOFTWARE: PatentIn Release #1.0, Version #1.30		
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	APPLICATION NUMBER: US/08/988,819		
	FILING DATE: 12-DEC-1997		
	CLASSIFICATION: 536		
	PRIOR APPLICATION DATA:		
	APPLICATION NUMBER: US 08/792,019		
	FILING DATE: 03-FEB-1997		
	ATTORNEY/AGENT INFORMATION:		
	NAME: COOK, ROBERT R.		
	REGISTRATION NUMBER: 31,602		
	REFERENCE/DOCKET NUMBER: A-442A		
	INFORMATION FOR SEQ ID NO: 1:		
	SEQUENCE CHARACTERISTICS:		
	LENGTH: 797 base pairs		
	TYPE: nucleic acid		
	STRANDEDNESS: single		
	TOPOLOGY: linear		
	MOLECULE TYPE: cDNA		
	FEATURE:		
	NAME/KEY: CDS		
	LOCATION: 90..764		
	FEATURE:		
	NAME/KEY: mat_peptide		
	LOCATION: 171..764		
	FEATURE:		
	NAME/KEY: sig_peptide		
	LOCATION: 90..170		
	US-08-988-819-1		
Query Match	81.7%	Score 669.4	DB 3: length 797.

Query Match	52.5%	Score 429.6;	DB 1;	Length 5087;
Best Local Similarity	90.4%;	Pred. No. 1.3e-103;		
Matches 459;	Conservative	0;	Mismatches 49;	Indels 0;
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Db	3423	CAGAGACTTGCCCAAGGGCCACTGTGACTTGGAGGTGTGGCGAAGCCTTAATGACAAAC	3482
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Oy	696	acttcaaacccggttlaagaagaagatgcagccctccagcagcttcagatcaacctgcacttgg	755
Db	3783	ACTTTCAACCGGCTCAAGAAGAAATGACGCTCCAGCAGCTGCAGTGCACCTGCACACTGG	3842
Oy	756	aggcacaatgtttctgcaccttgacct 783	
Db	3843	GGGCTCATGACTTCTGACTCTTGACCTT 3870	

RESULT 9
US-08-988-819-3
; Sequence 3, Application US/08988819
; Patent No. 6054294

COUNTRY: USA

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: PatentIn Release #1.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: IIS/08/9888.819

FILING DATE: 12-DEC-1997

PRIOR APPLICATION DATA: 00 0000 0100

APPLICATION NUMBER: 03-111-1000
FILING DATE: 03-FEB-1997

NAME: COOK, ROBERT R.
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 31,602
 EVIDENCE / DOCKET NUMBER: A-442A

INFORMATION FOR SEQ ID NO: 3:

LENGTH: 5087 base pairs

TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: Linear
MOTIF TYPE: DNA (genomic)

FEATURE:

LOCATION: 137..138

OTHER INFORMATION: REGI

3-6T8-986-80

525
526

est Local Similarity 90.4%

100

[illegible]

3363 AGCTGGAACTACCTGGGCCCCC

336 cagaactctgccagggccca

3423 CAGAGACTCTGCCCAGGGCC

396 tgcgctgaccgaactatg

3483 TCGGCTGACCCAGAACTACG

456 accatcaqctgccacagctg

3E43 AGCGGAGCCACTGGCTC

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3003 AGGGLC1GC1GGGC,CCCC

576 ctctgccagggaactgagcca

3663 CGCTGCCCTGGGACTGAACCC

636 agatgatgacttctgctg

3723 AGATGGACGACTTCTGGCTG

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Db 3783 ACTTCAACCGGCTCAAGAGAAAGATGAGCTCCAGCAGCTGAGTCAGCCACCTGG 3842
QY 756 aggcacatggtctctcagctcagcct 783
Db 3843 GGGCTCATGCTCTGACTTGTGACCTT 3870

RESULT 10

US-09-016-534-3
; Sequence 3, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULIA
; APPLICANT: SENALDI, GIORGIO
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/016,534
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5087 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 137..138
; OTHER INFORMATION: /product= "INTERVENING UNSEQUENCED"
; OTHER INFORMATION: REGION OF >1KB"
US-09-016-534-3

Query Match 52.5%; Score 429.6; DB 3; Length 5087;
Best Local Similarity 90.4%; Pred. No. 1.3e-103;

Matches 459; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 276 acctgaactcctggggccccccttcaacagagcgtcactcaatccctcagactggggg 335
Db 3363 AGCTGAACCTACTGGGCCCCCTTCAACGAGCAGACTTCAACCTCCCGCTGGGGG 3422
QY 336 cagaacctctcccaaggcccggtcacttggaagtgtggcgaagcctcaatgacagc 395
Db 3423 CAGAGACTCTGCCCCAGGGCCACTGTGACTTGAGGTGTGGCGAAGCCTCAATGACAAAC 3482
QY 396 tggcggtgaccacgaatataagagcgtacagtcacctcctgtgtactgtgtgctc 455
|||||

Db 3483 TCGGGGTGACCCAGAACTACGAGGCTTACAGCCACTTCTGTGTACTTCA 3542
QY 456 accgtcaagctggtccacagctgaactcagagctagcgtgagccacttclgtacagccctc 515
Db 3543 ACCGTCAAGGCTGCCACTCTGAGCTGCCCGCAGAGCTGTGGCCACTTCTGTCA 3602
QY 516 agggctcgtggtgagcattgcaagtgcagctgaggaagcgtgtgtacccactgcccagc 575
Db 3603 AGGGCTGTGGGACGATTCGCGGCGTCAATGAGCAAGCTGTGGGTACCCACTGCCAGC 3662
QY 576 ctctgcaaggagctgagcagcctggtgcccctggtcccaagtaacttccctcaga 635
Db 3663 CGGTGCTGTGGGAGCTGAACCCACTTGTGACTCTGGCCTGCCACAGTACTTCTCCAGA 3722
QY 636 agatgatgactctgtgctgtaagaagagctgcaagctgagcattgagcgttccagcaag 695
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QY 696 actcaaccggttaagaagaagatgacagctccagcagcctcagctcagctcagctgag 755
Db 3783 ACTTCAACCGGCTCAAGAGAAAGATGAGCTCCAGCAGCTGAGTCAGCCACCTGG 3842
QY 756 aggcacatggtctctcagctcagcct 783
Db 3843 GGGCTCATGCTCTGACTTGTGACCTT 3870
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RESULT 11

US-09-106-182-7
; Sequence 7, Application US/09106182
; Patent No. 6046035
; GENERAL INFORMATION:
; APPLICANT: Shi, Yangu
; APPLICANT: Ruben, Steve
; TITLE OF INVENTION: Cardiotrophin-Like Cytokine
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc
; STREET: 9410 Key West Ave
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/106,182
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/051,053
; FILING DATE: 30-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF385
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-106-182-7

Query Match

6.3%; Score 52; DB 3; Length 390;

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 204 gccctccatcagaaaactatgatcctaacgcgtactcgtag 247
 Db 6528 CCCCCCGCAGCTGTGCGCCCTGTGCCCCACCGCGAGAGCGCGCGC 6485

RESULT 14
 US-08-665-037-1
 : Sequence 1, Application US/08665037
 : Patent No. 5895813
 :
 : GENERAL INFORMATION:
 : APPLICANT: Seedorf, Klaus
 : APPLICANT: Ullich, Axel
 : TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
 : TITLE OF INVENTION: OF TKA-1 RELATED
 : TITLE OF INVENTION: DISORDERS
 : NUMBER OF SEQUENCES: 2
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : STREET: Suite 4700
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 90071-2066
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 : MEDIUM TYPE: storage
 : COMPUTER: IBM compatible
 : OPERATING SYSTEM: IBM P.C. DOS 5.0
 : SOFTWARE: Word Perfect 5.1
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 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/665,037
 : FILING DATE: June 13, 1996
 : CLASSIFICATION: 530
 :
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 60/005,167
 : FILING DATE: October 13, 1995
 :
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Warburg, Richard J.
 : REGISTRATION NUMBER: 32,327
 : REFERENCE/DOCKET NUMBER: 220/156
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (213) 489-1600
 : TELEFAX: (213) 955-0440
 :
 : TELEX: 67-3510
 :
 : INFORMATION FOR SEQ. ID NO.: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1642 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 :
 : FEATURE:
 : NAME/KEY: Coding Sequence
 : LOCATION: 97...1446
 :
 : US-08-665-037-1

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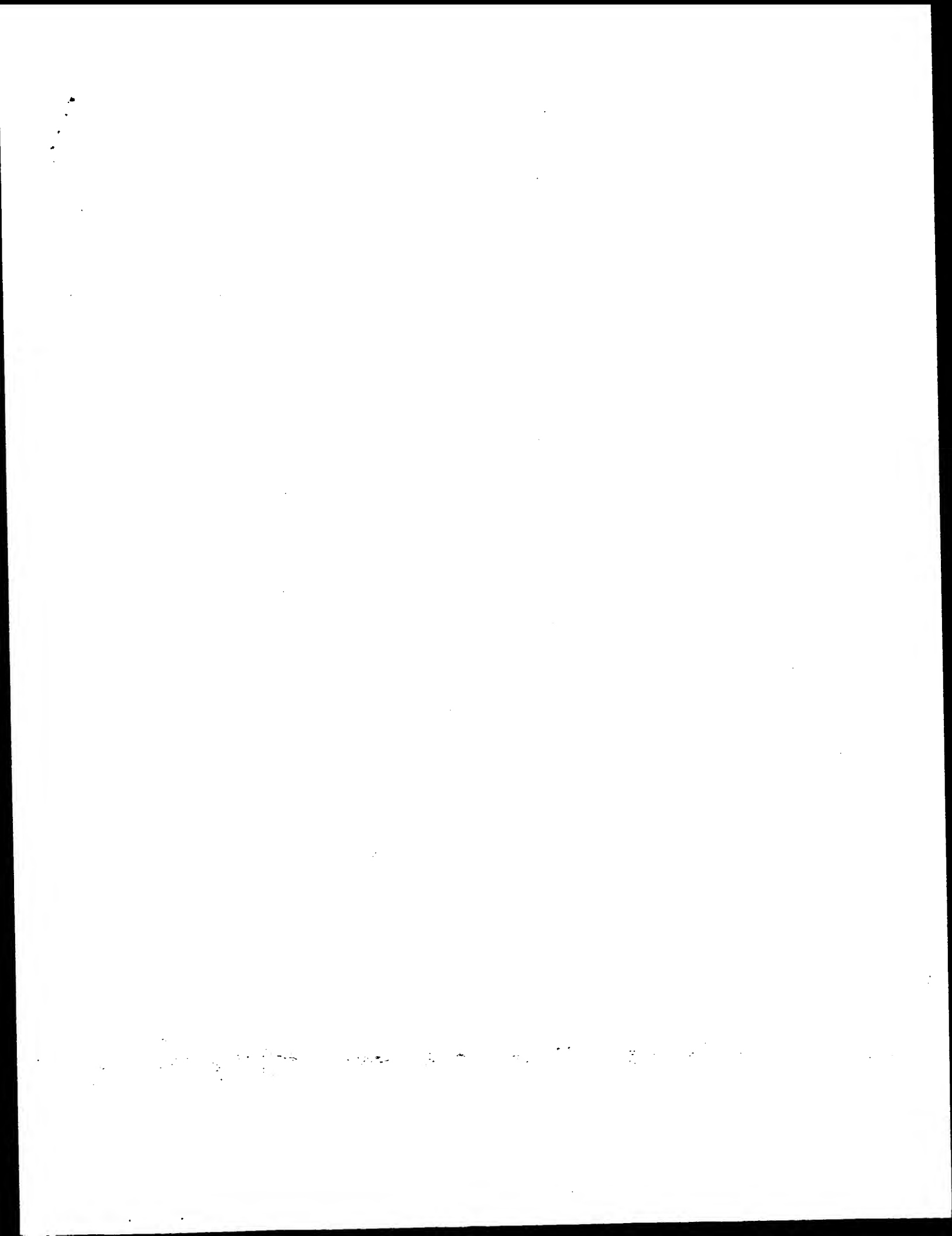
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Mon Mar 18 11:23:41 2002

us-09-931-704-4.rn1

Page 11

Search completed: March 18, 2002, 10:25:14
Job time: 2854 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:32:30 ; Search time 41.88 seconds
(without alignments)
409.247 Million cell updates/sec

Title: US-09-931-704-5
Perfect score: 1224
Sequence: 1 MDLRAGDSMGLACTVLM.....KKKQPPAAVTLHLEAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	118.5	9.7	203	JC4645	cardiotrophin-1 -
2	110.5	9.0	203	I49153	cardiotrophin-1 -
3	93.5	7.6	640	T34916	transferrin - Stre
4	92	7.5	332	G86182	hypothetical prote
5	91.5	7.5	201	G02312	cardiotrophin-1 -
6	90	7.4	195	JH0680	ciliary neurotroph
7	90	7.4	733	F82965	hypothetical prote
8	89	7.3	733	D83588	conserved hypothet
9	86	7.0	1313	T38943	probable guanine n
10	85.5	7.0	389	F72511	probable cystathio
11	85.5	7.0	560	C38604	poly(3-hydroxyalka
12	85	6.9	520	B75332	extracellular solu
13	84	6.8	741	A83271	hypothetical prote
14	83	6.8	272	T35231	hypothetical prote
15	83	6.8	272	T35231	zinc finger protei
16	83	6.8	955	T00247	zinc finger protei
17	83	6.8	1561	T00248	probable alpha-man
18	80.5	6.6	1006	T42762	TMV resistance pro
19	80	6.5	1179	T04584	hupk protein - Rho
20	79.5	6.5	294	S32947	hypothetical prote
21	79.5	6.5	316	T34553	activin receptor S
22	79.5	6.5	512	S21717	hypothetical prote
23	79.5	6.5	542	A82965	hypothetical prote
24	79.5	6.5	644	JC5119	anti-mulletian hor
25	79.5	6.5	1132	A35098	MHC class III hist
26	78.5	6.4	338	T45394	hypothetical prote
27	78.5	6.4	531	B83422	probable serine/th
28	78.5	6.4	571	H70623	probable potassium
29	78	6.4	1844	S01556	hypothetical prote
30	78	6.4	378	D83381	hypothetical prote

30	78	6.4	427	1	BRY655	non-directed DNA p
31	78	6.4	515	2	T37982	hypothetical prote
32	78	6.4	917	2	S40178	isoleucine-tRNA 1
33	77.5	6.3	572	2	B72714	probable methionyl
34	77.5	6.3	1182	2	I48378	hairless protein -
35	77	6.3	322	2	T23891	hypothetical prote
36	77	6.3	411	2	F75439	probable cell wall
37	77	6.3	1031	2	F83561	probable DNA polym
38	77	6.3	2261	1	A42548	glycine polypeptide
39	76.5	6.2	368	2	T51111	transferrin (
40	76.5	6.2	395	2	I49575	CCNA7/enhancer bin
41	76	6.2	232	2	E75547	hypothetical prote
42	76	6.2	508	2	A32225	novel growth facto
43	76	6.2	720	2	T36293	probable serine/th
44	76	6.2	812	2	T34180	hypothetical prote
45	76	6.2	891	2	H75507	hypothetical prote

ALIGNMENTS

RESULT 1

JC4645

cardiotrophin-1 - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000

C:Accession: JC4645

R:Shikawa, M.; Saito, Y.; Miyamoto, Y.; Kuwahara, K.; Ogawa, T.; Nakagawa, O.; Harad

Biochem. Biophys. Res. Commun. 219, 377-381, 1996

A:Title: cDNA cloning of rat cardiotrophin-1 (CT-1): Augmented expression of CT-1 gen

A:Reference number: JC4645; MUID:96193659

A:Accession: JC4645

A:Molecule type: mRNA

A:Residues: 1-203 <TS>

A:Cross-references: DDBJ:D78591; NID:g1256926; PIDD:BA11427 ; PID:g1256927

C:Genetics:

A:Gene: CT-1

C:Keywords: cardiac muscle; cytokine; heart

Query Match

Best Local Similarity 9.7%: Score 118.5; DB 2; Length 203;

Matches 49; Conservative 26; Mismatches 84; Indel 19; Gaps 6;

OY 40 IOKTYDITRYLEHQLRSIAGTYLNLGPPENEDPNPRL---GAETLPK...VMEYFWS 96

DB 27 IROTHNLARLLTKYADQLLEYVOGGEFGLPGFSPRLPLAGLSGPAF...NLLPV--- 83

OY 97 LNDRLRLTONYENYSHLCYRGLNRQA-----TAEIERSLAHFTSLGCIICSIAGVM 151

DB 84 -SERLR--QDAALASALPALDDAVARRQAEINPRAPRLRLSEDAARCAVRALGAATVTL 140

OY 152 ATIGY----PLPOPLPGTEPAWAPGPAHSDFLOKMDDEFWLKELOTWLR*NDENRL 205

DB 141 AALGAAGCPVEPV-ATSALEFTSNAGVSAKVLGLHVGGLGVEMVSRIT...DLGOL 197

RESULT 2

cardiotrophin-1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: I49153

R:Pennica, D.; King, K.L.; Shaw, K.J.; Luis, E.; Rullamas, I.; Hoh, S.; Darbonne, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1142-1146, 1995

A:Title: Expression cloning of cardiotrophin 1, a cytokine that induces cardiac myocy

A:Reference number: I49153; MUID:95166785

A:Accession: I49153

A>Status: nucleic acid sequence not shown; translated from cDNA

A:Molecule type: mRNA

A:Residues: 1-203 <RES>

A:Cross-references: EMBL:U18366; NID:g710331; PIDD:AAC5217 ; PID:g710332

C:Genetics:

RESULT 6
JH0680
Ciliary neurotrophic factor - chicken
N:Alternate names: growth-promoting activity protein
C:Species: Gallus gallus (chicken)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jul-2000
C:Accession: JH0680; PQ0057
C:Length: 1,045-1,053, 1992
N:Title: Cloning, expression during development, and evidence for release of a trophic factor
A:Reference number: JH0680; MUID:92304573
A:Accession: JH0680
A:Molecule type: mRNA
A:Residues: 1-195 <LEU>
A:Cross-references: GB:M60827; NID:g211822; PIDN:AAA48784.1; PID:g211823
A:Experimental source: eye
R:Eschenstein, F.P.; Esch, F.; Holbert, T.; Blacher, R.W.; Nishi, R.
Neuron 4, 623-631, 1990
A:Title: Purification and characterization of a trophic factor for embryonic peripheral
A:Reference number: PQ0057; MUID:90211978
A:Accession: PQ0057
A:Molecule type: protein
A:Residues: 155-166, 'X', 168-175 <ECK>
A:Experimental source: sciatic nerves
C:Comment: This is a neurotrophic protein.
C:Superfamily: ciliary neurotrophic factor
C:Keywords: growth factor

Query Match 7.4%; Score 90; DB 2; Length 195;
Best Local Similarity 27.7%; Pred. No. 0.48;
Matches 52; Conservative 21; Mismatches 83; Indels 32; Gaps 10;

OY 46 LTRYLEHQLSLAGTYLNTLGPFPNPPRLGAEITLPRATVNLVWRSLSNDRLRLTQ 105
DB 23 LARKMSDSDVLDLDIVVERG-----LDASISVAANDGVPTAAV--ERNAEQTGTORLDD 75
OY 106 N---YEAVSHLTCYLRGLNROA---ATAELRSLA-----HFCSTLGLGSLGSIAGVMA 152
DB 76 NLAAVRAFRFTLLQMLEEGRELLGDTDELGPALAMLLQVSAFYVHLEELT-----ELE 130
OY 153 TLGPIPLPQPLGTEPPAPASHPASDPLQKMDPWLKELQITWLMRSAXDNRLLKKMKOP 212
DB 131 SRGAPAE---GSEPP-AP-PRLSLPEQKLRGLRLRELQAWVRSVRLRLSK--HGP 183
OY 213 AASVTLHL 220
DB 184 GSCAALGL 191

RESULT 7
F82965
Hypothetical protein PA5441 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: F82965
C:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lm,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: A82950; MUID:20437337
A:Accession: F82965
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-733 <STO>
A:Cross-references: GB:AE004957; GB:AE004091; NID:99951770; PIDN:AG08826.1; GSPDB:GN001
C:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5441

Query Match 7.4%; Score 90; DB 2; Length 733;
Best Local Similarity 23.9%; Pred. No. 2.5;
Matches 48; Conservative 24; Mismatches 81; Indels 48; Gaps 8;

OY 23 PAVPALNRGTGDPGPGSIQKTYDITRLEHQLSLAGTYLNTLGPFPNPPRLGAEITL 82
DB 102 PALPAMSSEATPPAPAPSLAELAR-----OMGAE 132
OY 83 TLPRATVNLVWRSLSNDRLRLTONYEAVSHLTCYLRGLNROAATLELRLHFCSTSLQ 141
DB 133 ALPEKIGAEFFEGEGSRCSNDQSA---LAPLRQV-RDAGLGEATKALAN---SRL 184
OY 142 GLGSLGSIAGVMAATIGPIPLPQPLGTEPPAPASHPASDPLQKMDPWLKELQITWLMRSAXDNRLLKKMKOP 201
DB 185 DLGAGCGMEDEBELGCVLAQ---GVES--AAGKAFATYLEAANFYSGR--FDEAEG 224
OY 202 FNRLLKKMKOPPAASVTLHL 222
DB 235 FKALQDVSQLPWLKETALYLQA 255

RESULT 8
D83588
Conserved hypothetical protein PA0454 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83588
C:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lm,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: D83588
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-733 <STO>
A:Cross-references: GB:AE004483; GB:AE004091; NID:9994631; PIDN:AG03843.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0454
C:Superfamily: hypothetical protein H11680

Query Match 7.3%; Score 89; DB 2; Length 733;
Best Local Similarity 25.8%; Pred. No. 3.1;
Matches 57; Conservative 26; Mismatches 64; Indels 74; Gaps 13;

OY 28 LNRGTGDPGPGSIQKTYDITRLEHQLSLAGTYLNTLGPFPNPPRLGAEITL 77
DB 230 LNRIGHGRGPKV-----SRYLKVFIADVDYHERASSSHYNNRLAEATPISDVLFRQ 283
OY 78 RL-----GAETLPRATVNLVWRSLSNDRLRLTONYEAVSHLTCYLRGLNROAATLELRLHFCSTSLQ 131
DB 284 RLNLQGGKACQALARA-----IRLRQPPD-YA-----DL-LALEDLQA 320
OY 132 SLAHF---CTSLQGL---LGSAGVMAATIGPIPLPQPLGTEPPAPASHPASDPLQKMDPWLKELQITWLMRSAXDNRLLKKMKOP 184
DB 321 SLHLRQGSNPAWKGLRSLGALANILTLDRKL-----AGASNLIAIADDEQ 368
OY 185 FWLKELOITWLMRSAXD-FNRLLKKMKOPPAASVTLHL 224
DB 369 SALIDRSP---RSLKDAFERLRQQLP-----TSLFRHG 400

RESULT 9
T38943
Probable guanine nucleotide binding protein - fission yeast; Schizosaccharomyces pombe
C:Species: Schizosaccharomyces pombe
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38943
R:Skellon, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.; Paulsen, O.; V.

```
A;Map position: 1
```

148 LOGGLSIAGVMATLGYPLPQPL-PGTEPAWAPGPAHSDFLOKMDDEWLJKETWTWRS 198

machines 40; conservative 20; Mist

[illegible]

Db 363 LMY-----PSISRYVLPKPKVAAIAADLGAIGIKVNLKTEDWPKYLEDPRAGFGQATLY 418
QY 64 YLGPPEEPD-----FNPRPGAETLPRAVNLKLEWRSIN-DRLRLTON 106
Db 419 GMGGDYNDPDNFTSARYGDKGSDDIGFNG-----NILNTLNKGRALTOA 464
QY 107 YEAYSHLLCYLRGLNRQAATLRLSLAHECTSLG-----LLGSLAGVMTLG 155
Db 465 OKA-----PYKOLHELFTYANANVRLPLVHSTAAARITYKGMTGPTSLIVG 511

RESULT 13

hypothetical protein PA2984 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: AB3271
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lapid, K.; Lim,
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A:Reference number: AB2950; MUID:20437337
A:Accession: AB3271
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-741 <STO>
A:Cross-references: GB:AE004724; GB:AE004091; NID:99949083; PIDN:AA006372.1; GSPDB:GNO01
C:Genetics:
A:Gene: PA2984

Query Match 6.9%; Score 84; DB 2; Length 741;
Best Local Similarity 26.2%; Pred. No. 9;
Matches 64; Conservative 13; Mismatches 81; Indels 86; Gaps 13;

QY 5 AGDSW-----GMLACTGVNHLPAVPAVLRNRTGDPGPGPSIQKTYDRLRYLEHQLSLAGT 60
Db 447 AAAAASVALGMLGALC---WLAPA-----GLP-----LRALGAA 477
QY 61 YLNLGPPFNEPDPFNPRLGAETLPRAVNLKLEWRSIN-DRLRLTONYEASHLLCYLRG 119
Db 478 LL-----LPALLPSPPEWEG-----RAEVRVLDVGGLAVLVKRE-----HVLVDSG 522
QY 120 LNRQA-----TAELRRSLAHFCTSLGGLGSLAGVMTLGYP-----PQ 160
Db 523 A-RQGAADGGERVAVPYRLSLDLR-----LDGILLSHADNDHAGAPTVASRPV 573
QY 161 PLPTEPAPAPGAPSHSDFLQKMDFFMLKELQTLWMSAKDFNRLKKKMPAPASVTLHL 220
Db 574 WLVSSEPARLPPLFLFADSCDERSMSMDGVVEQWAMAQAGDSN-----DRSCVLRV 624
QY 221 EAHG 224
Db 625 EADG 628

RESULT 14

hypothetical protein SC5C7.24c SC5C7.24c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T35231
R:Seeger, K.J.; Harrell, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, September 1998
A:Reference number: 221572
A:Accession: T35231
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-272 <SEE>
A:Cross-references: EMBL:AL031515; PIDN:CAA20636.1; GSPDB:GN00070; SCOEDB:SC5C7.24c

A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC5C7.24c

Query Match 6.8%; Score 83; DB 2; Length 741;
Best Local Similarity 23.9%; Pred. No. 3.2;
Matches 38; Conservative 15; Mismatches 50; Indels 56; Gaps 7;

QY 23 PAVPALN-----RIGDPPGPGSIQKTYDRLRYLEHQLSLAGTYLNTY-----FN----- 70
Db 95 PALGALREKMERLIRGYEPYALVAVATYRVLANRGIAMLMGVASHLTL-----NATRLT 154
QY 71 -EPDPNPRLGAETLPRAVNLKLEWRSIN-DRLRLTONYEASHLLCYLRG 129
Db 155 LHPDGLAPRIR-----NLREMR-----GHL-----EOM 178
QY 130 RSLA-HFCTSLGGLGSLAGVMTLGYPPLPDPTEP 167
Db 179 ERQIALHRSRPLRELYDEVA-----AYPVESEVGAEP 211

RESULT 15

zinc finger protein w12 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 05-Nov-1999
C:Accession: T00247
R:Matsunoto, K.; Ishii, N.; Yoshida, S.; Shiosaka, S.; Watanabe, T.; Toyama, M.
submitted to the EMBL Data Library, March 1998
A:Description: Molecular cloning and distinct developmental expression pattern of spl
A:Reference number: Z14130
A:Accession: T00247
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-955 <MAT>
A:Cross-references: EMBL:AB012266; NID:d1227741; PIDN:BA032791.1; PID:d1033757
A:Experimental source: brain
C:Genetics:
A:Gene: w12

Query Match 6.8%; Score 83; DB 2; Length 955;
Best Local Similarity 27.0%; Pred. No. 15;
Matches 34; Conservative 20; Mismatches 48; Indels 41; Gaps 7;

QY 22 LPAVPAVNRGDPGPGPSIQKTYDRLRYLEHQLSLAG-----TYLNTYLP-----PFPNPD 73
Db 615 LPLSPPLASRPKPGAGPT-----QVPR--ELSLPITGSKPSASVGLVY-----KPLQEDR 667
QY 74 FNPRPGAETLPRAVNLKLEWRSIN-DRLRLTONYEASHLLCYLRG-----RQQAATAELR 130
Db 668 FLPAEVAKAKITYTETLPPKA-KTLHEK-----TSHSSTEACELGGLVPEVKKALASHAR 721
QY 131 RSLAHF 136
Db 722 AHLROF 727

Search completed: March 18, 2002, 09:32:32
Job time: 218 sec

QY 97 LNDRLRLTONYAYSHLLCYLRGLNRQA-----TAEIRSLAHFCTSLQGLGSIAGVM 151
 Db 84 -SERLR--ODAAALSLPALLDVARRQAEINRAPRLRSLEDAARQVRAALGAAYETVL 140
 QY 152 ATGCGY-----PLPDLPTGEPAMAPGPAHSDFLQKMDPFWLKEQLCTWLRSAKDNRL 205
 Db 141 AALGAAGAAGVPEPV-ATSALEFTSNAGVSAKVLGLHVCLYGEWVSRTSGDGLQL 197

RESULT 2

CTFL_MOUSE
 ID CTFL_MOUSE STANDARD: PRT: 203 AA.
 AC 060753;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE CARDIOTROPIN-1 (CT-1).
 GN CTFL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9516785; PubMed=7862649;
 RA Pennica D., King K.L., Shaw K.J., Luis E., Fullamas J., Luo S.-M.,
 RA Darbonne W.C., Knutson D.S., Yen R., Chien K.R., Baker J.B.,
 RA Wood W.I.;
 RT "Expression cloning of cardiostrophin 1, a cytokine that induces
 RT cardiac myocyte hypertrophy.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1142-1146(1995).
 CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
 CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
 CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
 CC LIVER, LUNG AND KIDNEY. LOWER LEVELS IN TESTIS AND BRAIN. NO
 CC EXPRESSION IN SPLEEN.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC EMBL; U18366; AAC52173.1;
 DR MGD; MGI:105115; Ctlf.
 DR CYLOKINE.
 KW
 SQ SEQUENCE 203 AA: 21509 MW: 883D414A0B3B232F CRC64;

Query Match 9.0%; Score 110.5; DB 1; Length 203;
 Best Local Similarity 27.4%; Pred. NO. 0.0023;
 Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IOKTYDRLRYLEHQLSLAGTYLNTYLGPPFNPPDPNPRRL--GAETLPRAVTVLEWRS 96
 Db 27 IROTHSLAHLLTKYARQQLQEEYVQOOGPEFFGLPGSPRLPLAGLSGAPSHAGLPV--- 83
 QY 97 LNDRLRLTONYAYSHLLCYLRGLNRQA-----TAEIRSLAHFCTSLQGLGSIAGVM 151
 Db 84 -SERLR--ODAAALSLPALLDVARRQAEINRAPRLRSLEDAARQVRAALGAAYETVL 140
 QY 152 ATGCGY-----PLPDLPTGEPAMAPGPAHSDFLQKMDPFWLKEQLCTWLRSAKDNRL 205
 Db 141 AALGAAGAAGVPEPV-ATSALEFTSNAGVSAKVLGLHVCLYGEWVSRTSGDGLQL 197

RESULT 3

CTFL_HUMAN
 ID CTFL_HUMAN STANDARD: PRT: 195 AA.
 AC 002011;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

ID CTFL_HUMAN STANDARD: PRT: 201 AA.
 AC 016619;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE CARDIOTROPIN-1 (CT-1).
 GN CTFL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX TISSUE=Heart;
 RX MEDLINE=96429882; PubMed=8833032;
 RA Pennica D., Swanson T.A., Shaw K.J., Kuang W.-J., Grollman
 RA Beatty B.G., Wood W.I.;
 RT "Human cardiostrophin-1: protein and gene structure, biological and
 RT binding activities, and chromosomal localization.";
 RL Cytokine 8:183-189(1996).
 CC -1- FUNCTION: INDUCES CARDIAC MYOCYTE HYPERTROPHY IN VITRO. BINDS TO
 CC AND ACTIVATES THE LEUKEMIA INHIBITORY FACTOR RECEPTOR (LIF
 CC RECEPTOR)/GP 130 RECEPTOR COMPLEX.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, SKELETAL MUSCLE,
 CC PROSTATE AND OVARY. LOWER LEVELS IN LUNG, KIDNEY, PANCREAS,
 CC THYMUS, TESTIS AND SMALL INTESTINE. LITTLE OR NO EXPRESSION IN
 CC BRAIN, PLACENTA, LIVER, SPLEEN, COLON OR PERIPHERAL BLOOD
 CC LEUCOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
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 CC EMBL; U43033; AAD12173.1;
 DR EMBL; U43031; AAD12173.1; JOINED.
 DR EMBL; U43032; AAD12173.1; JOINED.
 DR HSSP; P04002; AA85229.1;
 DR MIM; 600435;
 DR CYLOKINE.
 KW
 SQ SEQUENCE 201 AA: 21227 MW: 0235A7B5745F675F CRC64;

Query Match 7.5%; Score 91.5; DB 1; Length 201;
 Best Local Similarity 25.7%; Pred. NO. 0.14;
 Matches 45; Conservative 23; Mismatches 92; Indels 15; Gaps 5;

QY 40 IOKTYDRLRYLEHQLSLAGTYLNTYLGPPFNPPDPNPRRL--GAETLPRAVTVLEWRS 96
 Db 27 IROTHSLAHLLTKYARQQLQEEYVQOOGPEFFGLPGSPRLPLAGLSGAPSHAGLPV--- 83
 QY 100 RBLTTONYAYSHLLCYLRGLNRQA-----TAEIRSLAHFCTSLQGLGSIAGVM 151
 Db 86 RRLT--DAALALPRLPLLDVARRQAEINRAPRLRSLEDAARQVRAALGAAYETVL 140
 QY 155 GY-----PLPDLPTGEPAMAPGPAHSDFLQKMDPFWLKEQLCTWLRSAKDNRL 205
 Db 144 GAANGPRAEPAAVASA--ASATGVPAKVLGLRVCGYREWLSTREDDGLQL 195

RESULT 4

CTFL_CHICK
 ID CTFL_CHICK STANDARD: PRT: 195 AA.
 AC 002011;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE CILIARY NEUROTROPHIC FACTOR (CNTF) (GROWTH PROMOTING ACTIVITY) (GPA).
 GN CNF OR GPA.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92304573; PubMed=1610564;
 RA Leung D.W., Parent A.S., Cachianes G., Lee A.L., Nikolic K.,
 RA Esch F., Coulombe J.N., Blacher R.W., Eckenstein F.P., Nishi R.;
 RT "Cloning, expression during development, and evidence for release of
 a trophic factor for ciliary ganglion neurons."
 RL Neuron 8:1045-1053(1992).
 CC -1- FUNCTION: CNTF IS A SURVIVAL FACTOR FOR VARIOUS NEURONAL CELL
 CC TYPES. SEEMS TO PREVENT THE DEGENERATION OF MOTOR AXONS AFTER
 CC AXOTOMY.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM.
 CC -1- SIMILARITY: BELONGS TO THE CNTF FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M80827; AAA48784.1; -
 CC PIR: JH0680; JH0680.
 CC HSSP: P26441; ICNT.
 CC InterPro: IPR000151; CNTF.
 CC Pfam: PF01110; CNTF; 1.
 CC ProDom: PD011041; CNTF; 1.
 CC Growth factor; Neurone.
 CC SEQUENCE 195 AA; 21330 MW; FEA076949DB34AC5 CRC64;
 SQ
 Query Match 7.4%; Score 90; DB 1; Length 195;
 Best Local Similarity 27.7%; Pred. No. 0.19;
 Matches 52; Conservative 21; Mismatches 83; Indels 32; Gaps 10;
 QY 46 LTRVLEHQLRSAGTYLMLGPPNEPPNPRRLGAEPLPRATVLEWRSINDRLRLTQ 105
 DB 23 LARKKRSVYTLDLITYERQG-----IDASISVAADVDPPTAAV--ERWAEQTGTQRLID 75
 QY 106 N---YEAYSHLLCYLRGLNRQA---ATAELRRSLA-----HECTSLOGLGSLAGYMA 152
 DB 76 NLAAVRAFRLLLAQMLEQRELLDDTDAELGPALAAMLQYSAFYHLEELL-----ELE 130
 QY 153 TLGVPRLQPLRGTEPPANAPGAHSDFLQKMDFWLLKELQTLWMSAKDFNRLKKMKOP 212
 DB 131 SRGPAE---GSEPP-AP-PRLSLFQKRLKGLVRELAAVAVSVADLQLSK--HGP 183
 QY 213 AASVTLHL 220
 DB 184 GSGAALGL 191
 RESULT 5
 MIPL_SCHPO STANDARD; PRT; 1313 AA.
 AC P87141;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DE WD-REPEAT PROTEIN MIPL.
 GN MIPL OR SPAC57A7.11.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=20115869; PubMed=10648609;
 RA Shinozaki-Yabana S., Watanabe Y., Yamamoto M.;
 RT "Novel WD-repeat protein Miplp facilitates function of the meiotic
 RT regulator Mei2p in fission yeast."
 RL Mol. Cell. Biol. 20:1234-1242(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Skelton J., Churcher C.M., Wood V., Barrell B.G., Rajandram M.A.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ database.
 CC -1- FUNCTION: BINDS TO AND FACILITATES THE FUNCTIONING OF THE MEIOTIC
 CC REGULATOR MEI2. MAY ALSO BE INVOLVED IN CONUGATION BY INTERACTING
 CC WITH STE11. ESSENTIAL FOR CELL GROWTH.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB032552; BAA84585.1; -
 CC EMBL: Z95396; CAB08769.1; -
 CC InterPro: IPR001680; WD40.
 CC Pfam: PRO0400; WD40; 7.
 CC PRINTS: PR00320; GPROTEINRPT.
 CC SMART: SM00320; WD40; 5.
 CC PROSITE: PS00678; WD_REPEATS_1; 1.
 CC PROSITE: PS50082; WD_REPEATS_2; 2.
 CC PROSITE: PS50294; WD_REPEATS_REGION; 1.
 CC KW Meiosis; WD repeat; Repeat.
 CC FT REPEAT 986 1029 WD 1.
 CC FT REPEAT 1033 1074 WD 2.
 CC FT REPEAT 1087 1126 WD 3.
 CC FT REPEAT 1130 1170 WD 4.
 CC FT REPEAT 1176 1216 WD 5.
 CC FT REPEAT 1219 1259 WD 6.
 CC FT REPEAT 1268 1308 WD 7.
 CC SEQUENCE 1313 AA; 148533 MW; C71B63B0171E7A4 CRC64;
 SQ
 Query Match 7.0%; Score 86; DB 1; Length 1313;
 Best Local Similarity 22.2%; Pred. No. 4.9;
 Matches 58; Conservative 31; Mismatches 84; Indels 88; Gaps 12;
 QY 15 ICTVIMHLPAY--PALNR-----TGDPGPGPSI-----OKTVYVGLHQLRS 56
 DB 811 LAFLLQHPALHAKSLSKDPTNSVTSDBKPHFVPSVSENKILKRSFI--LSKGLIALS 870
 QY 57 LAG-----TYLNYL-----GPP-FNEPDPNPRRLGAEPLPRATVNL 91
 DB 871 LAGSDRASELLSINGENKPAESNLNHLTSAKVPAPPAEDELQY---SELIPLTSLYLF 926
 QY 92 EWMRSINDRLRLTONYEAYSHLLCYLRGL---NRQATAELRSLAHFCT---LQG 142
 DB 927 DMSKRYFTEPQMRNEDDEPGSCYNQRLMRNRNEKLIYTRPLAFV--LN--KNNQQLMT 986
 QY 143 LLGSLAGVMTLGYPLPPLRGTEPPANAPGAHSDFLQKMDFWLLKEL--TWLMSA 199
 DB 987 FNNRTIA-----PRKLTFQEFEDQLITLGGKII--VWDMWRN 1022
 QY 200 KDNRLKKMKOPPAASYTLHL 220
 DB 1023 RCINSFK-----TSASATTVV 1038

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GN HUPK.
OS Rhodopseudomonas capsulatus (Rhodospseudomonas capsulata).
CC Bacteria; Proteobacteria; alpha subdivision; Rhodobacteriales; Rhodobacter.
CX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9117783; PubMed=2007559;
RX Xu H.W., Wall J.D.;
RT "Clustering of genes necessary for hydrogen oxidation in Rhodospseudomonas capsulatus."
RL J. Bacteriol. 173:2401-2405(1991).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=B10;
RX STRAIN=B10;
RA MEDLINE=93268090; PubMed=8497190;
RX Delplanq A., Richard P., Toussaint B., Caballero F., Elstner C.,
RA Delplanq C., Smith R.L., Chabert J., Vignais P.M.;
RT "Organization of the genes necessary for hydrogenase oxidation in Rhodospseudomonas capsulatus. Sequence analysis and identification of two hyp regulatory mutants."
RL Mol. Microbiol. 8:15-29(1993).
CC -1. SIMILARITY: BELONGS TO THE HUPK FAMILY.
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CC EMBL: M55089; AAA72924.1;
DR EMBL: Z15089; CAA78803.1;
DR PIR: B38532; B38532.
DR PIR: S25691; S25691.
DR CONFLICT 70 A -> R (IN REF. 2).
FT SEQUENCE 294 AA; 30222 MW; 2669E8B70AF35EDA CRC64;
SQ
Query Match 6.9%; Score 84.5; DB 1; Length 111;
Best Local Similarity 31.2%; Pred. No. 1;
Matches 40; Conservative 3; Mismatches 38; Indel 47; Gaps 6
QY 76 PRLGATLRRAVYVLEWMSINDRLRLTQNYEAYSHLCYGLGNKQAVAR-----LRRS 132
DB 36 PPGVAELRLP-----LENLCAAGGHAARLAL-----GLPEVAPARRELROH 80
QY 133 IAHFCTSLQGLGSIAGVMATLGYRLPGTREPAPAPGPAHSDFLOKKMDDEWLKEIQ 192
DB 81 LAKICLIMPKRLGL-----AQQPLP-----EHWAEGGA-----ALQ 111
QY 193 TWLRSAR 200
DB 112 HMLWGAK 119

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RX MEDLINE-96117077; PubMed=8562059;
RA Okamura N., Tamba M., Liao H.-J., Onoe S., Sugita Y., Dacheux F.,
RA Dacheux J.-L.;
RT "Cloning of complementary DNA encoding a 135-kilodalton protein
RT secreted from porcine corpus epididymis and its identification as an
RT epididymis-specific alpha-mannosidase.";
RL Mol. Reprod. Dev. 42:141-148(1995).
CC -1- FUNCTION: CAN DIGEST BOTH P-NITRO-PHENYL-ALPHA-D-MANNOSIDE AND
CC HIGH MANNOSE OLIGO SACCHARIDE (MAN8)-GLUCNA(2)). MAY BE INVOLVED
CC IN SPERM MATURATION. HAS A POSSIBLE ROLE IN SPECIFIC SPERM-EGG
CC INTERACTION SINCE SPERM SURFACE MANNOSEDASE ACTS LIKE A RECEPTOR
CC FOR MANNOSE-CONTAINING OLIGOSACCHARIDES LOCATED ON THE ZONA
CC PELLUCIDA. OPTIMAL MANNOSEDASE ACTIVITY WAS FOUND AT PH 6.5.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING ALPHA-D-
CC MANNOSE RESIDUES IN ALPHA-D-MANNOSIDES.
CC -1- SUBCELLULAR LOCATION: SECRETED. FOUND AT THE SPERM SURFACE AS A
CC -1- TISSUE SPECIFICITY: SPECIFIC TO THE CAPUT AND CORPUS OF THE
CC EPIDIDYMIS.
CC -1- PTM: PROCESSED INTO A 27 KDA FRAGMENT LOCALIZED ON THE EQUATORIAL
CC SEGMENT AND THE APICAL RIM OF THE HEAD OF MATURE SPERM.
CC -1- SIMILARITY: BELONGS TO FAMILY 38 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL: D28521; BA005877.1;
DR InterPro: IPR000602; Glyco_hydro_38.
DR Pfam: PF01074; Glyco_hydro_38; 1.
KW Hydrolase; Glycosidase; Signal; Glycoprotein.
FT SIGNAL 1 32
FT CHAIN 33 1006 EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE.
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 604 604 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 668 668 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 744 744 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 804 804 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 886 886 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 988 988 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 956 956 D -> A (IN REF. 1; AA SEQUENCE).
FT SEQUENCE 1006 AA: 115311 MW: 0845F8086C991BCD CRC64;
SQ
Query Match 6.6%; Score 80.5; DB 1; Length 1006;
Best Local Similarity 23.0%; Pred. NO. 11;
Matches 45; Conservative 22; Mismatches 62; Indels 67; Gaps 9;
QY 50 LENO-----LNSLACTYLYNYLGPENEDFNPRIGAEYL-----PRATVNEVWMSL 97
DB 838 LQHRPVVFLRGLSTGYONGCPKRPQEPVTLPPSLHLQILSLPGKYSNHTVHLKLNQKG 897
QY 98 NDR-----LRLQNEAVSHLLCYLRGLNRQAATLRLRSLSLAHFTCSLQGLGSI 147
DB 898 HYRAKADDFRVLRLHLHLYEAGEH-----QALSRYVT-----LNLQSVLRGL 940
QY 148 AGVWATLGYPLPGLPSTEPAMAPRAHSDFLQKMDDFWLKELQTLWLRSAKFNK--L 205
DB 941 GSVYAAV-----EERSLST-----WDVNSLHRMSWMTEDGHHRRGS 976
QY 206 KKKMOP--AASTPLH 219
DB 977 SRRLPPLRGPVNTIH 992
RESULT 9
VPP3_HUMAN STANDARD: PRT: 830 AA.
ID VPP3_HUMAN

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DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin; 1.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS00299; UBIQUITIN_1; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
KW Repeat.
FT DOMAIN 17 77 UBIQUITIN-LIKE.
FT DOMAIN 202 207 POLY-PRO.
FT REPEAT 242 270 4 X 29 AA APPROXIMATE REPEATS.
FT REPEAT 415 443 1.
FT REPEAT 574 602 2.
FT REPEAT 608 636 3.
FT REPEAT 657 670 4.
FT DOMAIN 1132 AA; 119504 MW; E28CABA78C38DD18 CRC64;
SQ SEQUENCE

Query Match 6.5%; Score 79; DB 1; Length 1132;
Best Local Similarity 26.1%; Pred. No. 18;
Matches 46; Conservative 17; Mismatches 67; Indels 46; Gaps 11;

OY 23 PAVNALNRGDPGPGPSIOKTYDLRLRYLEHOLRLSLAGTYLWGLGPPNEDPDPNRLGAE 82
DB 261 PA-PEPNAPNHPSPAEVEVLQELQR-LESRLQPLQRYEVLGAAT-TYNNHGRE 317
OY 83 TLPRATVLEWRSLSNDRRLTQN-YEAYSHLYLRLGRLNQAAT---AEIIRSLAHFC 137
DB 318 EDQR-LINL-----VGEELRLGLMTFVALSPLRCNL-----ACPRPHLHVRRMSHYT 365
OY 138 TSLGGLGSLAGVWATLGYPL-----POPLRPT-PAWAGPAHS 176
DB 366 TPM-----VLQQAAPLPIQINWGTVTWTGNGTRPPPPNNAEAPPGCGQASS 412

RESULT 12
ATRA_MYCTU STANDARD; PRT; 571 AA.
AC P96371;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE POTASSIUM-TRANSPORTING ATPASE (EC 3.6.3.12) (POTASSIUM-TRANSLCATING ATPASE A CHAIN) (ATP PHOSPHOHYDROLASE [POTASSIUM-TRANSPORTING] A CHAIN) (POTASSIUM BINDING AND TRANSLCATING SUBUNIT A).
DE KOPA OR RV1029 OR MT1058 OR MTCY10G2.20C.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV.
RX MEDLINE=9825987; PubMed=9634230;
RA Cole S.T., Brosch R., Parhail J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagsels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers K., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
RT Nature 393:537-544(1998).
RL [12]
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Bishal A., Utterback T., Weidman J., Kouri H., Gill J., Mikula A.,

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RT "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains."
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ database.
RL -I- FUNCTION: ONE OF THE COMPONENTS OF THE HIGH-AFFINITY ATP-DRIVEN POTASSIUM TRANSPORT (OR KDP) SYSTEM, WHICH CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF HYDROGEN AND POTASSIUM IONS (BY SIMILARITY).
CC -I- CATALYTIC ACTIVITY: ATP + H(2)O + K(+)(OUT) = ADP + PHOSPHATE + K(+)(IN).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PRO-GLF).
CC -I- SIMILARITY: BELONGS TO THE KOPA FAMILY.
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CC EMBL: Z92539; CAB06850.1; -.
CC DR EMBL; AEO06988; AAK45310.1; -.
CC DR TIGR; MT1058; -.
CC DR Hydrolyase; Transport; Potassium transport; Transmembrane;
CC KW Complete proteome.
CC FT TRANSMEM 7 27 POTENTIAL.
CC FT TRANSMEM 66 86 POTENTIAL.
CC FT TRANSMEM 137 157 POTENTIAL.
CC FT TRANSMEM 188 208 POTENTIAL.
CC FT TRANSMEM 255 275 POTENTIAL.
CC FT TRANSMEM 286 306 POTENTIAL.
CC FT TRANSMEM 369 389 POTENTIAL.
CC FT TRANSMEM 390 410 POTENTIAL.
CC FT TRANSMEM 430 450 POTENTIAL.
CC FT TRANSMEM 497 517 POTENTIAL.
CC FT TRANSMEM 539 559 POTENTIAL.
CC FT SEQUENCE 571 AA; 60163 MW; 4A3238D1C62A3687 CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 1;
Best Local Similarity 22.9%; Pred. No. 8.7;
Matches 54; Conservative 31; Mismatches 76; Indels 75; Gaps 12;

OY 5 AGDSWGLACLTCTVLMHPAYPAL-----NRTGDPGPGPSIOK 46
DB 2 SGTSLQFRALIAVL--LTPALGGLYLAITYGDEAKKRGDVFGEIVTLCVNDG 59
OY 47 --TRYLEHQLRSLAGTYLNYL-----GPPNEDPDPNRLGAE 93
DB 60 SEQRSTVALSVLAFSVMSEFLLYGIALRPGVLPENPTD--KPAVTDHVA 117
OY 94 --WRSINDRLRLT-----QNYEASHLCTL-----RGINQQA 131
DB 118 TNWQSYSGEPAMSHFTQMTGLAVNFEVSASAGCVIALIRGLARKRAS 177
OY 132 SLAHCTSP-----QGLGSLAG-VMATLGYPLPQPLGTEPPAWA 176
DB 178 TYLRIMPLSFVALILVSGVYQIMLHGRTIVANTLEGARQLLPG----- 226

RESULT 13
POLR_TYMW STANDARD; PRT; 1844 AA.
AC P10358;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).
OS Turnip yellow mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage;
OX NCBI_TaxID=12154;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE-88289359; PubMed-3399388;
RA Morch M.D., Boyer J.C., Haenni A.L.;
RT "Overlapping open reading frames revealed by complete nucleotide
RU sequencing of turnip yellow mosaic virus genomic RNA.";
CC Nucleic Acids Res. 16:6157-6173(1988).
CC -1- MISCELLANEOUS: THE 206 KDA PROTEIN IS POTENTIALLY A POLYPEPTIDE
CC (BY HOMOLOGOUS TO THE LONGER PROTEIN OF THE SINDBIS VIRUS).
CC -----
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CC -----
DR EMBL: X07441; CAA30322.1; ALT_SEQ.
DR PIR: S01956; S01956.
DR MEROPS: C21.001; -.
DR InterPro: IPR000606; Viral_helicase1.
DR Pfam: PF01443; Viral_helicase1.
KM Transferase: RNA-directed RNA polymerase: Polypeptide: ATP-binding.
FT NP_BIND 976 983 ATP (BY SIMILARITY).
FT DOMAIN 1631 1663 POLYMERASE SITE (BY SIMILARITY).
SQ SEQUENCE 1844 AA; 206640 MW; A016D758C83D128C CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 1844;
Best Local Similarity 24.6%; Pred. No. 38;
Matches 57; Conservative 18; Mismatches 60; Indels 97; Gaps 13;

OY 7 DSMGMLACLCYVLMHPALNRTGDPGPGSID-----KTYDLTR-YLEHOLSLAGT 60
DB 237 ESMG-----PVHSLIORGTGTPRPPDSQAPRTMTSLDFRSYQGEPRLDVVS-- 282
OY 61 YLNLGPPNEPDNPRLGAETLPRAVNLVWRSLSLDRILRQNYAYSHLLCYRLGL 120
DB 283 -----FRIPD-----AIELPQATF---LQPLRDRVPRAYNA---LFYTR-- 319
OY 121 NROATAELRSLAHFCTSLQGLGSLAGVATLGYPLPPLGPEPAPGAPSAHSDPLQ 180
DB 320 -----AVRLRIS-----DPA-AVVRHMS---S 338
OY 181 KMDFWLLKELQTLWRSKXDFNRLKKMP-----PAASYTLHLLEAH 223
DB 339 KPDDHWTSN-----AMDNLQTFALLNVLPRNVVYHYLQSPLASLSTYLRLQH 386

RESULT 14
Y140_HUMAN STANDARD; PRT; 422 AA.
AC Q14153;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOPHYSICAL PROTEIN KIAA0140.
GN KIAA0140.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RX MEDLINE-96127530; PubMed-8590280;
RA Nagase T., Seki N., Tanaka A., Ishikawa K.-I., Nomura N.;
RT "Prediction of the coding sequences of unidentified human genes. IV.
RT The coding sequences of 40 new genes (KIAA0121-KIAA0160) deduced by
RT analysis of cDNA clones from human cell line KG-1.";
RL DNA Res. 2:167-174(1995).
CC -----
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CC -----
DR EMBL: D50930; BAA09489.1; -.
KM Hypothetical protein.
SQ SEQUENCE 422 AA; 45796 MW; 8F607F093408CEAC CRC64;

Query Match 6.4%; Score 78; DB 1; Length 422;
Best Local Similarity 21.6%; Pred. No. 6.6;
Matches 45; Conservative 21; Mismatches 74; Indels 68; Gaps 8;

OY 4 RAGDSWGMACLCYVLMHPALNRTGDPGPGSIDKTYDLTRYL-EHOLSLAGT 61
DB 206 QAGDWS-----PDLHPVG-----GRDLQSLSCSHQPS-----F 238
OY 62 LNYLGPPEPDNPRLGAETLPRAVNLVWRS-----LNR----- 100
DB 239 VEYCPSPANSIPASTPELA-----RRSSGLSRKSPQCVLNDKKVKKRP+EPQORP 293
OY 101 -----LRTQNEYAYSHLLCYLGLNRQAATLRLSLAHFCTSLQGLGSLAGVATLGY 156
DB 294 SLDLAKMAQNCQTFSSLCSLCSAGTEDCGPGSPFAHVSNTRAWLALLSASNGRTPAGT 353
OY 157 PLPPLPPTGTERPAMGAPSAHSDPLQKMD 184
DB 354 PVPEPLP-----PSFDHLVCOED 372

RESULT 15
RT65_MYXXA STANDARD; PRT; 427 AA.
ID P23071;
AC P23071;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA-DIRECTED DNA POLYMERASE FROM RETRON MX65 (EC 2.7.7.6) (NEVERSE
DE TRANSCRIPTION) (MX65-RT).
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacterales;
OC Myxococcales; Cytophasterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-90138993; PubMed-1689062;
RA Inouye S., Herzer P.J., Inouye M.;
RT "Two independent retrans with highly diverse reverse transcriptases
RT in Myxococcus xanthus.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:942-945(1990).
CC -1- FUNCTION: PARTICIPATES IN THE SYNTHESIS OF A MSDNA (A BRANCHED RNA
CC LINKED BY A 2',5'-PHOSPHODIESTER LINKAGE TO A SINGLE-STRANDED DNA)
CC OF UNKNOWN FUNCTION. THE RETRON TRANSCRIPT SERVES AS PRIMER AND
CC TEMPLATE TO THE REACTION, AND CODES FOR THE RT.
CC -1- CATALYTIC ACTIVITY: N-DEOXYNUCLEOSIDE TRIPHOSPHATE
CC N PYROPHOSPHATE + DNA(N) ->
CC -1- MISCELLANEOUS: M.XANTHUS CONTAINS TWO INDEPENDENT AND UNLINKED
CC RETRONS: MX65 AND MX162.
CC -1- MISCELLANEOUS: RETRONS MAY BE THE ANCESTORS OF RETROVIRUS.
CC -1- SIMILARITY: TO OTHER REVERSE TRANSCRIPTASES IN BACTERIA AND
CC RETROVIRUSES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----

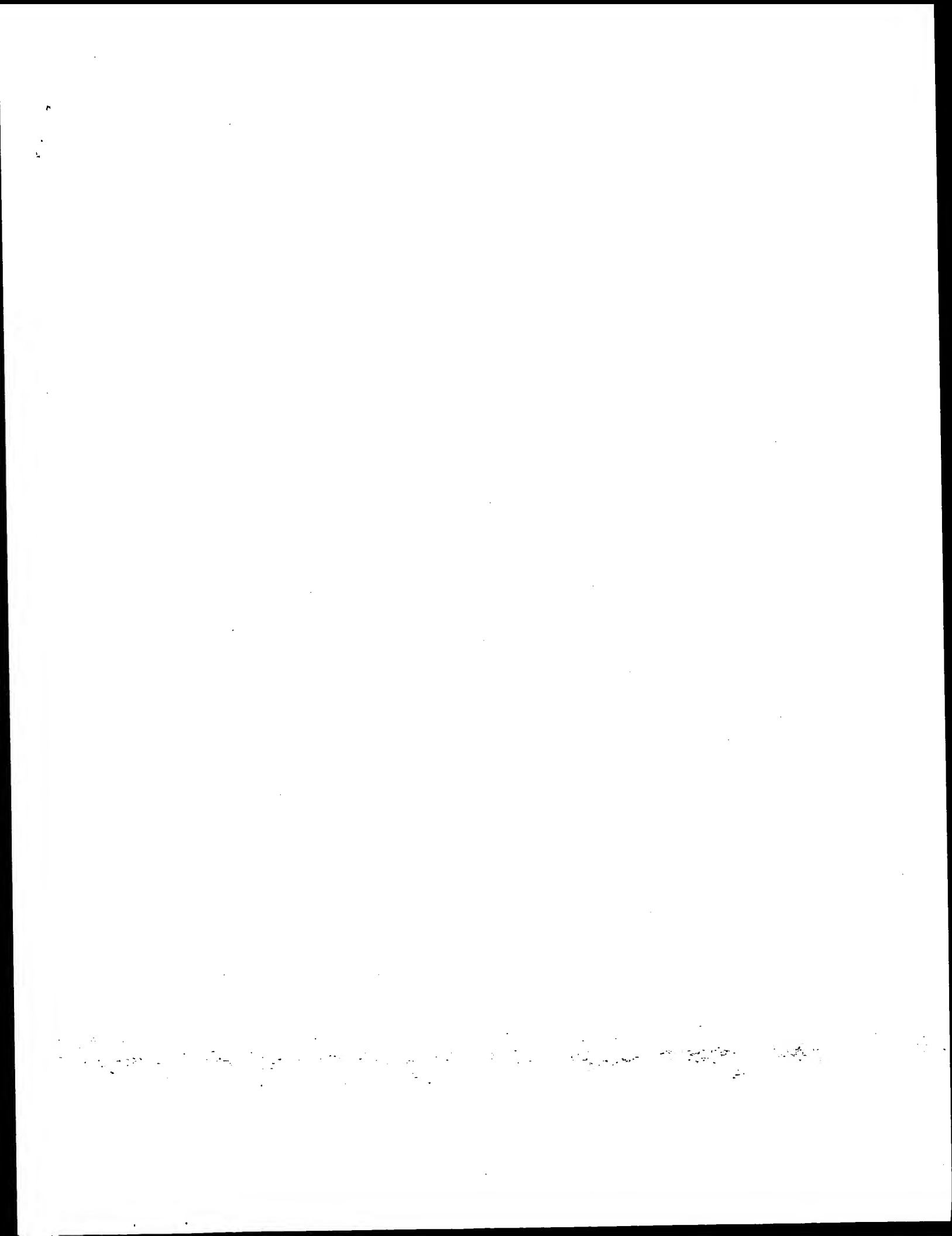
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DR EMBL; M30609; AAA88323.1; -.
 DR PIR; A34864; RRYC65.
 DR InterPro; IPR000123; RNA_DNAPolymS.
 DR InterPro; IPR000477; RYTSe.
 DR Pfam; PF00078; rvt; 1.
 DR PRINTS; PR00866; RNADNAPOLMS.
 KW Transferase; RNA-directed RNA polymerase; Transposable element.
 SQ SEQUENCE 427 AA; 48024 MW; C96436BF86E4DD7 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 427;
 Best Local Similarity 24.4%; Pred. No. 6.7;
 Matches 38; Conservative 23; Mismatches 53; Indels 42; Gaps 6;

QY 18 VLMHLPAPVPAALNRTGDPG-----PGPSIOKTYDITRYLE----- 51
 Db 266 ILFHVVPVGPVPCVQGAAPTSPALCNVALLRLDRRLAGLARRGYTYRYADDLTFSGDDVT 325
 QY 52 --HQLSLAGTYLNYIGPPNPDPNPRL-GAETLPRAVTNLEWRSNDRLRL----- 103
 Db 326 ALERVRALARYVOEGEFVNRKTRVQRRGAQRYTGVTNTTGLSRERPRRLRLMLH 385
 QY 104 ---TONYEAY-SH---LICYLRLGRLNRQAATFELRR 131
 Db 386 QEARSEDVEHRAHLDDLALAYVMLNPEOARLARR 421

Search completed: March 18, 2002, 09:40:14
 Job time: 530 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:39:15 ; Search time 75.65 seconds
(without alignments)
435,047 Million cell updates/sec

Title: us-09-931-704-5
Perfect score: 1224
Sequence: 1 MDLRAGDSWGMACCTYLW.....KKKMPASVTLHLAHGF 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTREMBL_17.*
2: sp.archaea.*
3: sp.bacteria.*
4: sp.fungi.*
5: sp.human.*
6: sp.invertebrate.*
7: sp.mammal.*
8: sp.mhc.*
9: sp.organelle.*
10: sp.phage.*
11: sp.plant.*
12: sp.rodent.*
13: sp.virus.*
14: sp.unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1224	100.0	225	11 09QZM3	Q9gzm3 mus musculu
2	1193	97.5	225	4 09UBP9	Q9ubp9 homo sapien
3	144.5	11.8	215	13 09PUJ2	Q9puj2 plethodon j
4	144.5	11.8	215	13 09PUJ1	Q9puj1 plethodon j
5	144.5	11.8	215	13 09PUJ0	Q9puj0 plethodon j
6	142.5	11.6	215	13 09PU19	Q9pu19 plethodon j
7	93.5	7.6	640	2 054153	054153 streptomyc
8	93	7.6	727	11 088841	088841 mus musculu
9	92	7.5	332	10 09MAU1	Q9mau1 arabidopsis
10	91.5	7.5	455	11 09CWV7	Q9cwv7 mus musculu
11	91	7.4	423	11 09JHE4	Q9jhe4 mus musculu
12	90	7.4	423	11 09JHE5	Q9jhe5 pseudomonas
13	89	7.3	423	11 09DBV6	Q9dbv6 mus musculu
14	89	7.3	733	2 091664	Q91664 pseudomonas
15	88	7.2	222	2 09L584	Q9l584 streptococ
16	87	7.1	1620	2 09Y4K6	Q9y4k6 homo sapien
17	86.5	7.1	1429	4 09HAV8	Q9hav8 homo sapien
18	86	7.0	559	4 09G799	Q9g799 homo sapien
19	86	7.0	619	4 09Q0L2	Q9q0l2 homo sapien

20	86	7.0	619	4 09UBU9	Q9ubu9 homo sapien
21	85.5	7.0	389	1 09YA71	Q9ya71 aeropyrum p
22	85.5	7.0	1154	11 09RT12	Q9rt12 mus musculu
23	85	6.9	520	2 09RT14	Q9rt14 deinococcus
24	85	6.9	585	5 09VNR6	Q9vnr6 atrophilia
25	84	6.9	741	2 09H2M0	Q9h2m0 pseudomonas
26	83	6.8	272	2 086721	Q86721 streptomyc
27	83	6.8	396	2 09AF00	Q9af00 frankia sp.
28	83	6.8	955	11 088287	Q88287 mus musculu
29	83	6.8	1561	11 088286	Q88286 mus musculu
30	82.5	6.7	1098	11 09WTN8	Q9wtm8 rattus norv
31	82.5	6.7	5990	2 09RLP6	Q9rlp6 mycobacteri
32	81.5	6.7	209	2 09LS93	Q9ls93 streptococ
33	81.5	6.7	256	2 09LS90	Q9ls90 streptococ
34	81.5	6.7	294	11 09CP21	Q9cp21 mus musculu
35	81	6.6	227	2 09KGS0	Q9kgs0 streptococ
36	81	6.6	237	2 09LS92	Q9ls92 streptococ
37	81	6.6	256	2 09LS94	Q9ls94 streptococ
38	81	6.6	395	2 09LAV9	Q9lav9 streptococ
39	81	6.6	1266	3 09ZCD2	Q9zcd2 neurospora
40	81	6.6	373	2 09ZGC0	Q9zgc0 streptomyc
41	80.5	6.6	373	2 09ZG4	Q9zg4 streptomyc
42	80.5	6.6	379	2 09ZG4	Q9zg4 streptomyc
43	80	6.5	294	4 09NXX5	Q9nxx5 homo sapien
44	80	6.5	876	4 09P210	Q9p210 homo sapien
45	80	6.5	1179	10 065507	Q65507 arabidopsis

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	225 AA.
09QZM3				
ID	09QZM3			
AC	Q9QZM3:			
DT	01-MAY-2000 (TREMBLrel. 13, Created)			
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	NEUROTROPHIN-1/B-CELL STIMULATING FACTOR-3.			
GN	BSF3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Muridae; Mus.			
OC	Mammalia; Eutheria; Rodentia; Muridae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=99432254; PubMed=10500198;			
RA	Serafini G., Varnum B.C., Sarmiento U., Starnes C., Liu			
RA	Guo J., Elliott G., McNinch J., Shalee C.L., Freeman L.			
RA	Simonet W.S., Boone T., Chang M.-S.,			
RT	"Novel neurotrophin-1/B cell-stimulating factor-3: A cy			
RT	II-6 family."			
RL	Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).			
DR	EMBL: AF176913; AF00993.1; -			
DR	MGD: MGI:1930088; Bsf3.			
SQ	SEQUENCE 225 AA; 25261 MW; 68B1FEABYFLA950 CRC61.			

Query Match	100.0%;	Score 1224;	DB 11;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.1e-110;		
Matches 225;	Conservative 0;	Mismatches 0;	Indel 0;	Gaps 0;
QY	1	MDLRAGDSWGMACCTYLWHLPAVPAALNRGDPGSPISQKTYDLTR	1	QKSLACT 60
DB	1	MDLRAGDSWGMACCTYLWHLPAVPAALNRGDPGSPISQKTYDLTR	1	QKSLACT 60
QY	61	YLVYLGPPPEPNDPFRGATLPRATVNTLVMSLNDRLRLQNFVAVS	61	LCYIRGL 120
DB	61	YLVYLGPPPEPNDPFRGATLPRATVNTLVMSLNDRLRLQNFVAVS	61	LCYIRGL 120
QY	121	NROAAFAELRSLAHPCSTLQGLGSIAGVMTLCPLPPLPTEPAAV	121	HSDFLO 180
DB	121	NROAAFAELRSLAHPCSTLQGLGSIAGVMTLCPLPPLPTEPAAV	121	HSDFLO 180

QY 181 KMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 225
 DB 181 KMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 225

RESULT 2

ID 09UBD9 PRELIMINARY: PRT: 225 AA.

AC 09UBD9: PRELIMINARY: PRT: 225 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE NEUROTOPHIN-1/B-CELL STIMULATING FACTOR-3.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

SEQUENCE FROM N.A.

RA Sendai G., Varnum B.C., Sarmiento U., Starnes C., Lille J., Scully S.,

RA Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Mann F.,

RA Simonet W.S., Boone T., Chang M.S.,

RT "Novel neurotrophin-1/B cell-stimulating factor-3: A cytokine of the

Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).

SEQUENCE FROM N.A.

RA MEDLINE=93382254; Pubmed=10448081;

RA Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J.,

RT "Computational EST database analysis identifies a novel member of the

neurotrophic cytokine family."

Biochem. Biophys. Res. Commun. 262:132-138(1999).

EMBL: AF172654; AAD54284.1; -

EMBL: AF176911; AAF00991.1; -

SEQUENCE 225 AA; 25176 MW; E2DD4B628083B55 CRC64;

Query Match

Best Local Similarity 97.5%; Score 1193; DB 4; Length 225;

Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACLTCTVHLPAVPAVLRTPGPGPSTQKTYDRLRYEHLQRLSLAGT 60

DB 1 MDLRAGDSWGLACLTCTVHLPAVPAVLRTPGPGPSTQKTYDRLRYEHLQRLSLAGT 60

QY 61 YLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 120

DB 61 YLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 120

QY 121 NROGAATAEELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 180

DB 121 NROGAATAEELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 180

QY 181 KMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 225

DB 181 KMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 225

RESULT 3

Q9PUJ2 PRELIMINARY: PRT: 215 AA.

AC 09PUJ2: PRELIMINARY: PRT: 215 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE RECEPTIVITY FACTOR ISOFORM 1 PRECURSOR.

GN Plethodon jordanii (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;

OC NCBI_TaxID=8336;

SEQUENCE FROM N.A.

RA MEDLINE=99420364; Pubmed=10489368;

RA Rollmann S.M., Houck L.D., Feldhoff R.C.;

RT "Proteinaceous pheromone affecting female receptivity in

salamander."

Science 285:1907-1909(1999).

EMBL: AF181481; AAF01026.1; -

EMBL: AF181481; AAF01026.1; -

SEQUENCE 215 AA; 24080 MW; B341B87B4E28438 CRC64;

Query Match

Best Local Similarity 11.8%; Score 144.5; DB 13; Length 215;

Matches 41; Conservative 31; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 115

DB 56 SLAGTYLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 115

QY 116 YLR-GLNRO----ATAELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 170

DB 116 YLR-GLNRO----ATAELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 170

QY 171 PGPAHSDFLQKMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 212

DB 171 PGPAHSDFLQKMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 212

RESULT 4

Q9PUJ1 PRELIMINARY: PRT: 215 AA.

AC 09PUJ1: PRELIMINARY: PRT: 215 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE RECEPTIVITY FACTOR ISOFORM 2 PRECURSOR.

GN Plethodon jordanii (Salamander).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;

OC NCBI_TaxID=8336;

SEQUENCE FROM N.A.

RA MEDLINE=99420364; Pubmed=10489368;

RA Rollmann S.M., Houck L.D., Feldhoff R.C.;

RT "Proteinaceous pheromone affecting female receptivity in

salamander."

Science 285:1907-1909(1999).

EMBL: AF181481; AAF01026.1; -

EMBL: AF181481; AAF01026.1; -

SEQUENCE 215 AA; 24080 MW; B341B87B4E28438 CRC64;

Query Match

Best Local Similarity 11.8%; Score 144.5; DB 13; Length 215;

Matches 41; Conservative 31; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 115

DB 56 SLAGTYLVYLGPPPEPPENPPRGAETLPRAVTVLEWRSLSLDRLLTQNYEAYSHLLCYLRGL 115

QY 116 YLR-GLNRO----ATAELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 170

DB 116 YLR-GLNRO----ATAELRSLAHFCTSLQGLGSIAGVMTIGVPLPQPRGPPAARPAASDFLQ 170

QY 171 PGPAHSDFLQKMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 212

DB 171 PGPAHSDFLQKMDDEWLKELQTWLWRSKADFNRLKKKMPAASVTLHLLEAHGF 212

Db 173 PFGSAIFRKKLRGGVCKEYKERVLTFRDFFELAKKYQ 212

RESULT 5

09PU10 PRELIMINARY; PRT; 215 AA.

AC 09PU10; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE RECEPTIVITY FACTOR ISOFORM 3 PRECURSOR.
 GN PRF.
 OS Plethodon jordani (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Kollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial salamander."
 RL Science 285:1907-1909(1999).
 DR EMBL: AF181482; AAF01027.1; -
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 215 AA; 24024 MW; 6BB6E4AD93A1343 CRC64;

Query Match 11.8%; Score 144.5; DB 13; Length 215;
 Best Local Similarity 26.5%; Pred. No. 3.4e-06;
 Matches 44; Conservative 34; Mismatches 73; Indels 15; Gaps 4;

QY 56 SLAGTYLNTLGPENEPDNPRLGAEPLPRATVNLVWRSINDRLRLTONYEAYSHLLC 115
 DB 55 SLPTLYLSFGAPLSDPDYQLPHIKVNLPTAMDYDTFRQTDERRKNNLYFSAYIE 114
 QY 116 YLR-----GLN--RQAATALRLSLAHCSTSLGSLGSIAGVATLGYPLPPLGTE 166
 DB 115 FLKEAMTEQEDLNPALALAKKEEAMANSNT---LISKISIDIMQMSVTILP--K 168
 QY 167 PAMAPGPAHSDFLOKMDDFMLKELQTLWLRSAKDNRLKKMKQP 212
 DB 169 PLVPPKGSAYFSKRLGGVCKEYKERVLTFRDFFELAKKYQ 214

RESULT 6
 09PU10 PRELIMINARY; PRT; 215 AA.
 AC 09PU10; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE RECEPTIVITY FACTOR ISOFORM 4 PRECURSOR.
 GN PRF.
 OS Plethodon jordani (Salamander).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Plethodontidae;
 OC Plethodon.
 OX NCBI_TaxID=8336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99420364; PubMed=10489368;
 RA Kollmann S.M., Houck L.D., Feldhoff R.C.;
 RT "Proteinaceous pheromone affecting female receptivity in a terrestrial salamander."
 RL Science 285:1907-1909(1999).
 DR EMBL: AF181483; AAF01028.1; -
 KW Signal.
 FT SIGNAL 1 23 POTENTIAL.
 SQ SEQUENCE 215 AA; 24054 MW; AAA412135FRA4E7F CRC64;

Query Match 11.6%; Score 142.5; DB 13; Length 215;
 Best Local Similarity 25.3%; Pred. No. 5.3e-06;
 Matches 41; Conservative 33; Mismatches 81; Indels 7; Gaps 3;

QY 56 SLAGTYLNTLGPENEPDNPRLGAEPLPRATVNLVWRSINDRLRLTONYEAYSHLLC 115
 DB 55 SLPTLYLSFGAPLSDPDYQLPHIKVNLPTAMDYDTFRQTDERRKNNLYFSAYIE 114
 QY 116 YLR-----GLN--RQAATALRLSLAHCSTSLGSLGSIAGVATLGYPLPPLGTE 170
 DB 115 FLKEAMTEQEDLNPALALAKKEEAMANSNTLISKISIDIMQMSVTILP--KPLV 172
 QY 171 PPAHSDFLOKMDDFMLKELQTLWLRSAKDNRLKKMKQP 212
 DB 173 PFGSAIFRKKLRGGVCKEYKERVLTFRDFFELAKKYQ 214

RESULT 7

054153 PRELIMINARY; PRT; 640 AA.

AC 054153; 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE TRANSFERASE.
 GN SCF7.10.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteriales;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A3(2);
 RA Oliver K., Harris D.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A3(2);
 RA Parkhill J., Barrall B.G., Rajandream M.A.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=A3(2);
 RA Redenbach M., Kleser H.M., Denapate D., Eichner A.;
 RA Kineshi H., Hopwood D.A.;
 RT "A set of ordered cosmid and a detailed genetic map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL021409; CA016181.1; -
 DR HSSP: P12998; IBS0.
 DR InterPro: IPR001917; AminoTransf.2.
 DR InterPro: IPR003880; Phosphotransf.2.
 DR Pfam: PF00222; aminotran_2; 1.
 DR ProSITE: PS50075; ACP_DOMAIN; 1.
 KW Phosphotransferase; Transferase.
 SQ SEQUENCE 640 AA; 68061 MW; E619FB5E55A613F CRC64;

Query Match 7.6%; Score 93.5; DB 2; Length 140;
 Best Local Similarity 28.3%; Pred. No. 1.1; Indels 57; Gaps 9;
 Matches 52; Conservative 12; Mismatches 63; Indels 57; Gaps 9;

QY 22 LPVAPALNRFGDGPSPISQIKTYDRLTYDEHOL---SLAGTYLNTLGPENEPDNPRLGAEPLPRATVNLVWRSINDRLRLTONYEAYSHLLC 140
 DB 100 LPVAPR-EGTGDPVTEAVVAAMKQTOYORHQLGADLEG-----E 140
 QY 79 LGAETTPRATVNLVWRSINDRLRLTONYEAYSHLLC 138
 DB 141 LGVDSVLTSTVAEA---TERLGLT-----GAAPDA 179

QY 142 GLLGAGVATLGGYPLPQPLPTGPAPWAPASDELQKMDPWLKELQTMWLRSAKD 201
 Db 185 DLGACGMEQDELGGVLAQ---GVES--AAGKATATLEAANFYSSR-----FDEAEQG 234
 QY 202 ENRLKKMKOPPAASVTLHLER 222
 Db 235 FKALQDVSOPLWELKETALYLQA 255

RESULT 13
 Q9D8V6
 ID 09D8V6 PRELIMINARY; PRT; 423 AA.
 AC 09D8V6;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE CEREBROSIDE (3'-PHOSPHOADENYLISULFATE:GALACTOSYLCERAMIDE 3')
 DE SULFOTRANSFERASE.
 GN CST.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=PANCREAS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schmitt L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarts P.,
 RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszynski A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
 RA Hayashizaki Y.
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 408:685-690(2001).
 DR EMBL; AK007645; BAB25160.1;
 DR MGI; MGI:1858277; Cst.
 SO SEQUENCE 423 AA; 48824 MW; 045303CECE150A3 CRC64;

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 Best Local Similarity 23.1%, Pred. No. 1.8;
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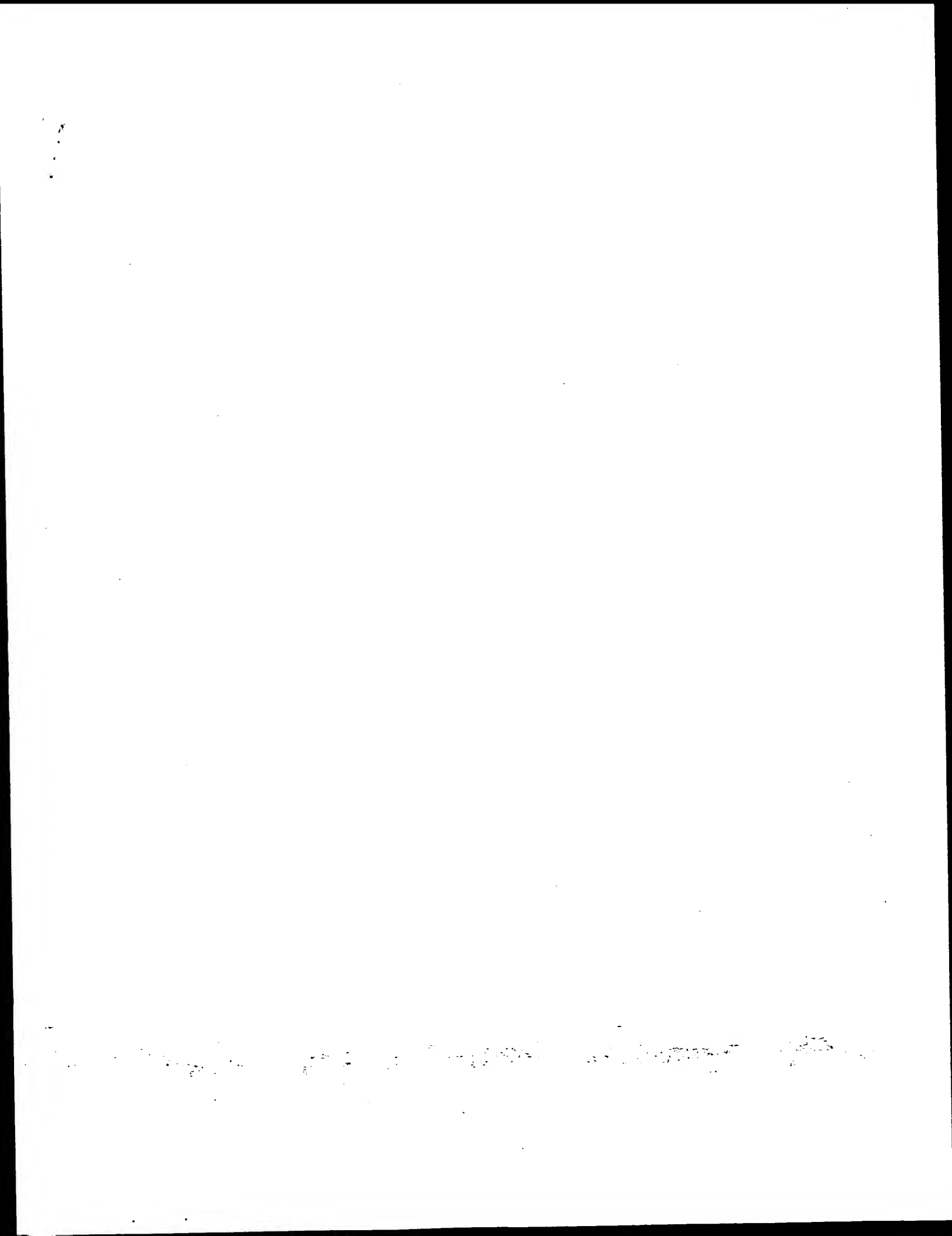
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 Db 264 ELLCWDLDKDVLYFKTLNARSDPVRRLSGELYRAT-----ANLLD---VLKRNHNASFWR 317
 QY 114 LCYLRGLNROA-ATAELRRS---LAHCTSLQGLGISA-----GVWATLGP 157
 Db 318 KVEAFGERARAEVAAELQAQENHRHICIDOGAVGAELADSDAMQWOPGLGKISILGYN 377
 QY 158 LPQPLPTGPAPWAPASDELQKMDPWLKELQTMWLRSAKD 201
 Db 378 LKRSI-----GPGHEDLCRGM---LTPLEIQLSDICGANLWTKMKPLRDELR 422

RESULT 14
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 ID 091664 PRELIMINARY; PRT; 733 AA.
 AC 091664;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE HYPOTHETICAL PROTEIN PA0454.
 GN PA0454.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OC Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PA01;
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Burkholder P.,
 RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik I.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
 RA Brady L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RL Nature 406:959-964(2000).
 DR EMBL; AE004483; AAG03843.1;
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 733 AA; 81538 MW; 580F9DBCB3909DB CRC6;

Query Match 7.3%, Score 89; DB 2; Length 77;
 Best Local Similarity 25.8%, Pred. No. 3.6;
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QY 28 LNRGTGPGPGPSIQTVDLFRYLE-----HQLRSLAGTYLVNLTGPVPRNLD--FNPP 77
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 QY 78 RL-----GATLPRATVNLVWRSINDRLRTQNEAVSHLQCYLNKI NGQAAVLELR 131
 Db 284 RLWQGGKACALARA-----ITLRQFPD-YA-----DRELALDLQA 320
 QY 132 SLAHF-----CTSLQGL-----LGSINGVATLGGYPLPQPLPTGPAPWAPASDELQKMD 184
 Db 321 SLHLRQGSNPAWKKGLRLSGALAAANLTIDRL-----AGASNPALADEOD 368
 QY 185 FWLKEQLQTMWLRSAKD-FNRLKKMKOPPAASVTLHLER 224
 Db 369 SALDRSP-----RSLKDAFERLRQQLTP-----TSLFRHG 400

RESULT 15
 Q9L584
 ID 09L584 PRELIMINARY; PRT; 222 AA.
 AC 09L584;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
 DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
 DE PSPA (FRAGMENT).
 GN PSPA.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=43;
 RA Beall B.W.;
 RT "PSPA sequence types from multiresistant pneumococci."
 RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF255543; AAF68096.1;



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:30:21 ; Search time 55.47 Seconds

(without alignments)
300.460 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224

Sequence: 1 MDLRAGDSWGMALACTVLW.....KKKMPAPASVTLHEAHGF 225

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1224	100.0	225	19 AAW29716	Mouse neurotrophic
2	1224	100.0	225	19 AAW56142	Amino acid sequenc
3	1224	100.0	225	21 AAW87814	Murine NNT-1 prote
4	1193	97.5	225	19 AAW29715	Human neurotrophic
5	1193	97.5	225	19 AAW56141	Amino acid sequenc
6	1193	97.5	225	20 AAW94466	Human cardiotoxiph
7	1193	97.5	225	21 AAW97813	Human NNT-1 protei
8	1193	97.5	225	22 AAW63543	Amino acid sequenc
9	1193	97.5	225	22 AAW5831	Human cardiotoxiph
10	1181	96.5	223	22 AAW00828	Human protein sequ
11	1167	95.3	215	21 AAW19587	Mouse interleukin-

12	1136	92.8	215	21 AAW19586	Human interleukin-
13	852	69.6	164	22 AAW20115	Peptide #6549 enco
14	852	69.6	164	22 AAW34012	Peptide #8049 enco
15	156.5	12.8	208	20 AAW09197	Human DNAX interle
16	154	12.6	208	20 AAW09196	Human DNAX interle
17	110.5	9.0	203	16 AAW3965	Mouse cardiac hype
18	110.5	9.0	203	17 AAW8204	Human cardiotoxiph
19	110.5	9.0	203	17 AAW8204	Murine cardiotoxiph
20	92.5	7.6	243	22 AAW29237	Human interleukin
21	92	7.5	332	21 AAG22132	Arabidopsis thalia
22	92	7.5	332	21 AAG40321	Arabidopsis thalia
23	91.5	7.5	201	16 AAW3967	Human cardiac hype
24	91.5	7.5	201	18 AAW29238	Human cardiotoxiph
25	91.5	7.5	201	20 AAW06490	Human tumour-assoc
26	91.5	7.5	201	21 AAW27662	Human protein PRO8
27	91.5	7.5	201	21 AAW13004	Human cardiotoxiph
28	91.5	7.5	201	21 AAW3697	Amino acid sequenc
29	91.5	7.5	201	21 AAW87818	Human cardiotoxiph
30	91.5	7.5	201	22 AAW50994	Human cardiotoxiph
31	90	7.4	195	14 AAW34432	Human PRO82 prote
32	90	7.4	195	20 AAW8337	Sequence of growth
33	87	7.1	242	22 AAW20275	Chicken ciliary ne
34	85.5	6.7	1473	22 AAW06758	Human interleukin
35	82.5	6.7	241	16 AAW76166	Human G-protein co
36	81.5	6.7	348	22 AAW84996	Human novel trans
37	81.5	6.7	352	14 AAW41000	Human brain CDNA c
38	81.5	6.6	379	21 AAW77185	S. venezuelae deso
39	81	6.6	379	21 AAW77208	S. venezuelae deso
40	80.5	6.6	620	21 AAW77179	S. venezuelae deso
41	80.5	6.6	3782	21 AAW77179	S. venezuelae deso
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43	79.5	6.5	350	22 AAW95861	Human protein sequ
44	79.5	6.5	350	22 AAW03542	Human protein kina
45	79.5	6.5	631	21 AAW43285	Human ORFX ORF3049

ALIGNMENTS

RESULT 1	
ID	AAW29716 standard; Protein; 225 AA.
AC	AAW29716;
XX	
DT	09-NOV-1998 (first entry)
XX	
DE	Mouse neurotrophic factor NNT-1.
XX	
KW	NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant;
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW	amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW	peripheral neuropathy; dystrophy; neural retina degeneration;
KW	common variable immunodeficiency; CVID; selective iga deficiency;
KW	hypogammaglobulinemia; X-linked agammaglobulinemia; anisepptic;
XX	
OS	Mus sp.
XX	
XX	
FT	Key
FT	Peptide
FT	Protein
XX	
XX	W09833922-A1.
XX	
XX	06-AUG-1998.
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XX	02-FEB-1998;
XX	
XX	30-JAN-1998;
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PR	03-FEB-1997;

Location/Qualifiers
1..27
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XX (AMGE-) AMGEN INC.
 PA Chang M, Elliott GS, Sarmiento U, Senaldi G;
 PI WPI; 1998-437475/37.
 DR N-PSDB; AAV47512.
 XX
 XX Newly isolated nucleic acid encoding human or murine neurotrophic
 PT factor NNT-1 - useful for treatment of neurological and
 PT immunological diseases or inflammation, also as vaccine adjuvant
 PS
 XX Claim 13; Fig 5; 120pp; English.
 XX
 CC This is the amino acid sequence of a murine neurotrophic factor,
 CC designated NNT-1, that is a growth factor for neurons and for B or
 CC T cells. It was deduced from isolated NNT-1 cDNA (see AAV47512).
 CC Human NNT-1 (see AAM29715) is also provided. Vectors and host cells
 CC for use in the production of human murine recombinant NNT-1
 CC polypeptides. These are used to treat: (i) neurological or
 CC immunological diseases, specifically Alzheimer's, Parkinson's
 CC or Huntington's diseases, amyotrophic lateral sclerosis,
 CC Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and
 CC degeneration of the neural retina, or conditions characterised by T
 CC or B cell defects, e.g. common variable immunodeficiency (CVID),
 CC selective Iga deficiency, hypogammaglobulinaemia and X-linked
 CC agammaglobulinaemia (claimed), but many others not disclosed; and (ii)
 CC inflammation. NNT-1 is also able to boost immunoreactivity and
 CC antibody production following vaccination, and, since it inhibits
 CC tumour necrosis factor production, it may also be useful for
 CC treating sepsis. In addition, cells that have been engineered to
 CC express NNT-1 can be implanted, or nucleic acids are delivered in
 CC gene therapy vectors.
 CC
 XX Sequence 225 AA:
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Query Match 100.0%; Score 1224; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.6e-121;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 mdlragsdwgmalcctctvlmhpavpalnrtgdpgpsigkcydltrylehnlrsag 60
 QY 61 YLNYLGPPEFNEPDPNPRIGAEETLPRAVNLKRWRSINDRLRLTONYEAVSHLCTLRGL 120
 DB 61 ylnylgppfnepdpnprigaeetlpratvnlkewrsindrlrltonyeavshlcytrgl 120
 QY 121 NRQATAEELRSLAHFCTSLQGLIGSTAGYMATLGYPLDPLPTEPMAWPGAHSDFLQ 180
 DB 121 nrqaataeellrslahfctslqgligstagymatlgyplpplptepwpgahsdflq 180
 QY 181 KMDDFWLKELQTMWLRSAKDFNRLKKMKOPPAASVTLHEAHGF 225
 DB 181 kmddfwwlkelqtmwlrskdfnrlkkmkppaasvvlheahgf 225

RESULT 2
 AAM56142
 ID AAM56142 standard; Protein: 225 AA.
 XX
 AC AAM56142;
 XX
 DT 13-JUL-1998 (first entry)
 XX
 DE Amino acid sequence of murine neurotrophic factor NNT-1.
 XX
 KW Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
 KW treatment; neurologic disease; degeneration; Parkinson's disease;
 KW amyotrophic lateral sclerosis; ALS; Alzheimer's disease; stroke.
 XX
 OS Mus sp.

XX Key Location/Qualifiers
 FH Peptide 1..27
 FT Protein /note= "signal peptide"
 FT Protein 28..225
 FT Protein /note= "mature peptide"
 XX
 XX US5741772-A.
 XX
 XX 21-APR-1998.
 XX
 XX 03-FEB-1997; 97US-0792019.
 XX
 XX 03-FEB-1997; 97US-0792019.
 XX
 XX (AMGE-) AMGEN INC.
 XX
 XX Chang M;
 XX
 XX WPI; 1998-260526/23.
 XX
 XX N-PSDB; AAV22654.
 XX
 XX Claim 2; Fig 5; 41pp; English.
 XX
 CC The present sequence represents a murine neurotrophic factor designated
 CC NNT-1, which is capable of stimulating growth of motor or sympathetic
 CC neurons. The NNT-1 protein is useful in the treatment of neurological
 CC diseases characterised by the degeneration and death of particular
 CC classes of neurons. These diseases specifically include Parkinson's
 CC disease, amyotrophic lateral sclerosis (ALS), Alzheimer's disease,
 CC stroke and various degenerative disorders affecting the brain.
 CC
 XX Sequence 225 AA:
 SQ

Query Match 100.0%; Score 1224; DB 19; Length 225;
 Best Local Similarity 100.0%; Pred. No. 1.6e-121;
 Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMALCTCTVLMHLPAPALNRTGDPGPGSTOKTYDITRYLEHOLSLAGT 60
 DB 1 mdlragsdwgmalcctctvlmhpavpalnrtgdpgpsigkcydltrylehnlrsag 60
 QY 61 YLNYLGPPEFNEPDPNPRIGAEETLPRAVNLKRWRSINDRLRLTONYEAVSHLCTLRGL 120
 DB 61 ylnylgppfnepdpnprigaeetlpratvnlkewrsindrlrltonyeavshlcytrgl 120
 QY 121 NRQATAEELRSLAHFCTSLQGLIGSTAGYMATLGYPLDPLPTEPMAWPGAHSDFLQ 180
 DB 121 nrqaataeellrslahfctslqgligstagymatlgyplpplptepwpgahsdflq 180
 QY 181 KMDDFWLKELQTMWLRSAKDFNRLKKMKOPPAASVTLHEAHGF 225
 DB 181 kmddfwwlkelqtmwlrskdfnrlkkmkppaasvvlheahgf 225

RESULT 3
 AAY87814
 ID AAY87814 standard; Protein: 225 AA.
 XX
 AC AAY87814;
 XX
 DT 24-AUG-2000 (first entry)
 XX
 DE Murine NNT-1 protein.
 XX
 KW NNT-1; neurotrophic factor; neurotrophic; neuroprotective; treatment;
 KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
 KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine;
 KW

KM	Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW	retinopathy; immune disorder; hematopoietic disorder.
XX	
OS	Mus sp.
XX	
PN	US6054294-A.
XX	
PD	25-APR-2000.
XX	
PF	12-DEC-1997; 97US-0988819.
XX	
PR	03-FEB-1997; 97US-0792019.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Chang M;
XX	
DR	WPI: 2000-338492/29.
DR	N-PSDB: AAA39483.
PT	New nucleic acids encoding neurotrophic factors useful for stimulating
PT	growth of motor or sympathetic neurons for treating neuron cell damage
PT	-
XX	
PS	Claim 2b: Fig 5; 42pp; English.
XX	
CC	This invention describes a novel nucleic acid molecule (I) encoding a
CC	novel neurotrophic factor (NNT-1) (II) which has nootropic,
CC	neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC	ophthalmological activity. (I) is useful for producing NNT-1
CC	polypeptides which are useful for treating patients in whom various
CC	cells of the central, autonomic, or peripheral nervous system have
CC	degenerated and/or have been damaged by congenital disease, trauma,
CC	mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC	disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC	proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC	amputrotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC	disease, peripheral neuropathy induced by diabetes or other metabolic
CC	disorders, and/or dystrophies or degeneration of the neural retina such
CC	as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC	night blindness, progressive cone-rod degeneration, immune disorders and
CC	hematopoietic disorders. (I) is effective in treating neurological
CC	conditions and promotes neuron regeneration. Neural functions are
CC	effectively restored in patients suffering from various neurological
CC	disorders. This sequence represents the murine NNT-1 protein described in
CC	the method of the invention.
XX	
SQ	Sequence 225 AA:
	Query Match 100.0%; Score 1224; DB 21; Length 225;
	Best Local Similarity 100.0%; Pred. No. 1.6e-121;
	Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 MDLRAGDSGMLACCTVLMHLPAVPALNRKTDPPGGPSIQTKTYDLTRLEQLSLACT 60
Db	1 mdlragsdsgmllactctvlwhlpavpalnrldppgppsikqtktydltrylenqlslagt 60
QY	61 YNYNGPPENEEDFNPRLRGAEFLPRATVNLEVMWSLNDRLNTONYEAYSHLLCYRL 120
Db	61 ynyngppeneedfnprlrgaelpratvnlewmwslnrdlntonyeyashllcyrl 120
QY	121 NRQAATAELRRSLAFCSTSLGLGSIAGVMA TLGYPLRPOLPGTEHPAPA PGPAHSDFLO 180
Db	121 nrqaataelrrslahfcts lgl lgs iagvm tly gplrpqpgtehpapapahsdflq 180
QY	181 KMDDEFLKLKETWLWRSAKDFNRLKKKQPAASTTLHEAHGF 225
Db	181 kmddewllkeltwtlwrsakdfnrlkkkmppaasttlheahgf 225

ID	AAW29715 standard; Protein; 225 AA.
AC	AAW29715;
XX	
DT	09-NOV-1998 (first entry)
XX	
DE	Human neurotrophic factor NNT-1.
XX	
KM	NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; peripheral neuropathy; dystrophy; neural retina degeneration; common variable immunodeficiency; CVID; selective IgA deficiency; hypogammaglobulinaemia; x-linked agammaglobulinaemia; antispleic therapy.
KM	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..27
FT	/label= Sig-peptide
FT	28..225
FT	Protein /label= Mat_protein
XX	
PN	MO9833922-A1.
XX	
PD	06-AUG-1998.
XX	
PF	02-FEB-1998; 98WO-US02363.
XX	
PR	30-JAN-1998; 98US-0016534.
PR	03-FEB-1997; 97US-0792019.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Chang M., Elliot GS, Sarmiento U, Senaldi G;
XX	
DR	WPI; 1998-437475/37.
XX	
DR	N-PESDB; AAW47510-11.
XX	
PT	Newly isolated nucleic acid encoding human or murine neurotrophic factor NNT-1 - useful for treatment of neurological and immunological diseases or inflammation, also as vaccine adjuvant
PS	Claim 12; Fig 3; 120pp; English.
XX	
CC	This is the amino acid sequence of a novel neurotrophic factor, designated NNT-1, that is a growth factor for neurons A, for B or T cells. It was deduced from isolated cDNA (see AAW47510) and genomic DNA (see AAW47511) clones. Vectors containing the cDNA or genomic DNA and host cells are provided for use in the production of NNT-1 polypeptides. These are used to treat: (i) neurological or immunological diseases, specifically Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and degeneration of the neural retina, or conditions characterised by T or B cell defects, e.g. common variable immunodeficiency (CVID), selective IgA deficiency, hypogammaglobulinaemia and X-linked agammaglobulinaemia (claimed), but many others disclosed; and (ii) inflammation. NNT-1 is also able to boost immunoreactivity and antibody production following vaccination, and, since it inhibits tumour necrosis factor production, it may also be useful for treating sepsis. In addition, cells that have been engineered to express NNT-1 can be implanted, or nucleic acids are delivered in gene therapy vectors.
CC	
SQ	Sequence 225 AA;
XX	
Query Match	97.5%; Score 1193; DB 19; Length .25;
Best Local Similarity	96.9%; Pred. No. 3e-118;
Matches 218; Conservative	3; Mismatches 4; Indels 0; Gaps 0;

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DQ      1 mdlragswgmglactctvlmhlpavpaplntgdpqpgpslqktydlrtylehnqlrsagt 60
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DQ      61 ylnylgpfnepdnprlgaetlpraatvnlqvwrsndrlrltonfeayshllcylrgl 120
QY      121 NROAATAEELRSLAHFCTSLQGLLGSTAGVMAATGYPPLPGLPETERAPAMPASDFLQ 180
DQ      121 nroaataeelrslahfctslqglilgstagvmaatgypplpglptepcwprpashdflq 180
QY      181 KMDFWLKLELQETWLMRSADKDFNRLKKMKQPPASVTLHLHANGF 225
DQ      181 kmddfwlkleglqetwlmrsakdfnrlkkmkppaavtlhghgaf 225

RESULT 5
AAW56141
ID      AAW56141 standard; Protein; 225 AA.
AC      AAW56141;
XX      13-JUL-1998 (first entry)
DE      Amino acid sequence of human neurotrophic factor NNT-1.
XX      Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron;
XX      treatment; neurological disease; degeneration; Parkinson's disease;
XX      amyotrophic lateral sclerosis; ALS; Alzheimers' s disease; stroke.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
XX      FT      Peptide      1..27
XX      FT      Protein      /note="signal peptide"
XX      FT      Protein      28..225 /note="mature protein"
XX      US5741772-A.
XX      21-APR-1998.
XX      03-FEB-1997; 97US-0792019.
XX      03-FEB-1997; 97US-0792019.
XX      (AMGE-) AMGEN INC.
XX      Chang M;
XX      WPI: 1998-260526/23.
XX      N-PSDB; AAV22652.
XX      Neurotrophic factor NNT-1 polypeptide and related nucleic acids -
XX      useful for stimulating growth of motor and sympathetic neurons
XX      Claim 1; Fig 3; 41pp; English.
XX      The present sequence represents a human neurotrophic factor, designated
XX      NNT-1, which is capable of stimulating growth of motor or sympathetic
XX      neurons. The NNT-1 protein is useful in the treatment of neurological
XX      diseases characterised by the degeneration and death of particular
XX      classes of neurons. These diseases specifically include Parkinson's
XX      disease, amyotrophic lateral sclerosis (ALS), Alzheimers's disease,
XX      stroke and various degenerative disorders affecting vision.
XX      Sequence      225 AA.

```

Query Match 97.5%; Score 1193; DB 19; Length 225;
 Best Local Similarity 96.9%; Pred. No. 3e-118; 4; Indels 0; Gaps 0;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

```

QY      1 MDLRAGDSWGMGLACTCTVLMHLPAPVAPALNRTGDPGPGPSIQKTYDTRTYLEHQRLSAGT 60
DQ      1 mdlragswgmglactctvlmhlpavpaplntgdpqpgpslqktydlrtylehnqlrsagt 60
DQ      61 YLNYLGGPFNEPDNPRLGAETLPRAATVNLQVWRSNDRLRLTONFEAYSHLLCYLRGL 120
DQ      61 ylnylgpfnepdnprlgaetlpraatvnlqvwrsndrlrltonfeayshllcylrgl 120
QY      121 NROAATAEELRSLAHFCTSLQGLLGSTAGVMAATGYPPLPGLPETERAPAMPASDFLQ 180
DQ      121 nroaataeelrslahfctslqglilgstagvmaatgypplpglptepcwprpashdflq 180
QY      181 KMDFWLKLELQETWLMRSADKDFNRLKKMKQPPASVTLHLHANGF 225
DQ      181 kmddfwlkleglqetwlmrsakdfnrlkkmkppaavtlhghgaf 225

RESULT 6
AAW94466
ID      AAW94466 standard; Protein; 225 AA.
AC      AAW94466;
XX      22-APR-1999 (first entry)
DE      Human cardiotrophin-like cytokine protein.
XX      Human; cardiotrophin-like cytokine; interleukin 6 cytokine family;
XX      CLC; IL-6; diagnosis; detection; immune system-related disorder;
XX      cancer; cardiac disorder; heart failure; hypertension; cancer;
XX      autoimmune disorder; infection.
XX      Homo sapiens.
XX      Key      Location/Qualifiers
XX      FT      Peptide      1..27
XX      FT      Protein      /label= signal
XX      FT      Protein      28..225 /label= Cardiotrophin-like_cytokine
XX      FT      Domain      74..79 /label= CD-I
XX      FT      Domain      /note="conserved domain"
XX      FT      Domain      150..156 /label= CD-II
XX      FT      Domain      /note="conserved domain"
XX      FT      Domain      194..198 /label= CD-III
XX      FT      Domain      /label= CD-III
XX      FT      Domain      /note="conserved domain"
XX      WO9900415-A1.
XX      07-JAN-1999.
XX      29-JUN-1998; 98WO-US13129.
XX      30-JUN-1997; 97US-0051311.
XX      (HUMA-) HUMAN GENOME SCI INC.
XX      Ruben SM, Shi Y;
XX      WPI: 1999-095678/08.
XX      N-PSDB; AAX16161.
XX      New isolated cardiotrophin-like cytokine nucleic acid - used to
XX      develop products for treating cardiac and immune system disorders,
XX      e.g. heart failure, hypertension, cancers, autoimmune disorders and
XX      infections
XX      Claim 1; Fig 1; 103pp; English.
XX      The present invention relates to a novel cardiotrophin-like cytokine

```

Query Match 97.5%; Score 1193; DB 19; Length 225;
 Best Local Similarity 96.9%; Pred. No. 3e-118; 4; Indels 0; Gaps 0;
 Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

CC (CLC) protein which is a member of the interleukin 6 (IL-6) cytokine
CC family. The present sequence represents the human CLC protein. The
CC present invention also describes screening methods for identifying
CC agonists and antagonists of CLC activity, as well as methods for
CC detecting cardiac and immune system-related disorders and
CC therapeutic methods for treating cardiac and immune system-related
CC disorders, e.g heart failure, hypertension, cancers, autoimmune
CC disorders and infections.

	Query Match	Best Local Similarity	97.55	Score 1193	DB 20	Length 225
Matches	218	Conservative	3	Mismatches	4	Indels
						Gaps
QY	1	MDLRAGDSWGLACLTCTVLMHLPAVPALNRTGDPGPGSIQKTYDLYRLEHOLRSIAGT	60			
Db	1	mdlragsdswgmhlacitcvtlwhlpavpalnrtcgdpqpgpsiqkydltcrylenhqlrslagt	60			
QY	61	YLNTLGPENFEDDNPPLGAEETLEPRATVNLKWRSLNDRLLRLTQNYEAVSHLLCYRGL	120			
Db	61	ylntlpgpenfeddnppplgaetlepratvnlkwrslndrllrltqnyeavshllcylrgl	120			
QY	121	NROQATAELRSLAHFCTSLQGLIGLSIAGWATATGYLPPQLPCTEPPAMPGPAHSFQL	180			
Db	121	nrgataelrslahfctslqglilgstlaaymaaylppqlpctepctppgpaahsfql	180			
QY	181	KMDFWLKLEQTQWLRMSAADFNRLKKRMQPPAASVTLLEAHGF	225			
Db	181	kmdfwllkeltqtwlrmsaadfnrlkkkmpapaavvllhgaahgf	225			

This invention describes a novel nucleic acid molecule (i) encoding a novel neurotrophic factor (NNT-1) (ii) which has neurotrophic, neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and ophthalmological activity. (i) is useful for producing NNT-1 polypeptides which are useful for treating patients in whom various cells of the central, autonomic, or peripheral nervous system have degenerated and/or have been damaged by congenital disease, trauma, mechanical damage, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to treat diseases like Alzheimer's, Parkinson's, amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral neuropathy induced by diabetes or other metabolic disorders, and/or dysretinopathies or degeneration of the neural retina such as retinitis pigmentosa, drug-induced retinopathies, stationary forms of night blindness, progressive cone-rod degeneration, immune disorders and hematopoietic disorders. (i) is effective in treating neurological and hematopoietic disorders and promotes neuron regeneration. NNT-1 effectively restored in patients suffering from various neurological disorders. This sequence represents the human NNT-1 protein described in the method of the invention.

Query Match	97.5%	Score 1193;	DB 21;	Length 25;
Best Local Similarity	96.9%	Pred. No. 3e-118;		
Matches 218;	Conservative 3;	Misses 4;	Indels 0;	Gaps
QY	1	MDLRAGDSWGLACLTCTVLMHLPAVPALNRRGDGPGPSIQKTYDTRVLEHQLRSLAGT	60	
Db	1	mlnrragdswwglacitctvlmhlpavpalnrrgtgdpqpslsktydtrvlehlrlslag	60	
QY	61	YLYNTYGPEFNPEDNPPLGAEETLPRAATVNLDEWRSLSNDELRLQNTQNEATSHLTCYRGL	120	
Db	61	yllyntygpefnpepnpplgaeltlpraatvnldewrslnsklrlrqneyeashllycyrql	120	
QY	121	NRGAATAELRRSLAHCFTSLQGLGSLAGWATAGYLPOLPCTEPMAMPNCPAHSFLO	180	
Db	121	nrgaataelrrslahcftslqgllyslagwaaqlylpplpqtptcepmvhpahsfliq	180	
QY	181	KMDPFVLLKTELQETWALNMSAKQFNELKRRKQMPAASVYLHLHAEFGF	225	
Db	181	kmddfvlkkelqetwawlnmsakqfnlkkkmpaavaevlhlhgafg	225	

Db 89 ylnylgppfnepdnpprlgaetlprativdewrslncklrltqneyashllcylrlg1 148
 QY 121 NRQAATLEKRLSLAHFCTSLQGLIGSIAGVWATLGYPLPQPLPCTEPAMAGPAHSDFLQ 180
 Db 149 nrgataeltrslahfctslqglislagymaalgyrlpqlpctepwlpghpsdflq 208
 QY 181 KMDFWLTKELQTLWMSAKDFNRLKKMKQPPAASVTLHEAHGF 225
 Db 209 kmddfllkeltqlwlrskdfrlkkmqppaaavclhlgahgf 253

RESULT 10

AAE00828
 ID AAE00828 standard; Protein; 223 AA.
 AC AAE00828;

DT 02-JUL-2001 (first entry)

XX Human cardiotrophin-like cytokine (CLC) protein.

XX Human: biologically active complex; haemopoietin receptor; NR6;
 KW cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
 XX differentiation; cell survival; neurotrophic activity.

OS Homo sapiens.

XX Key Location/Qualifiers
 FH Peptide 1..27
 FT /label= Signal_peptide
 FT Protein 28..223
 FT /label= Human_mature_CLC_protein
 FT /note= "Cardiotrophin-like cytokine"

XX W0200127157-A1.

XX 19-APR-2001.

XX 06-OCT-2000; 2000WO-AU01216.

XX 08-OCT-1999; 99AU-0003327.

XX 12-MAY-2000; 2000AU-0007489.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PI Nash A, Jachno KM, Fabri LJ, Reid K, Bartlett PF, Hilton DJ,
 PI Nakata Y, Hasegawa M;

DR WPI: 2001-281978/29.
 DR N-PSDB: AAD04201.

XX New biologically active complex comprising NR6 and
 PT cardiotrophin-like cytokine, for facilitating proliferation,
 PT differentiation and/or survival of a cell

XX Claim 32; Page 114-115; 123pp; English.

XX The present invention relates to a biologically active complex comprising
 CC a haemopoietin receptor, NR6 and cardiotrophin-like cytokine (CLC).
 CC The complex is useful in the manufacture of a medicament for the
 CC treatment and/or prophylaxis of a subject, as it is involved in
 CC facilitating proliferation, differentiation and/or survival of a cell.
 CC The complex or its components have neurotrophic activity. The present
 CC sequence is human cardiotrophin-like cytokine (CLC) protein.

XX Sequence 223 AA;

Query Match 96.5%; Score 1181; DB 22; Length 223;
 Best Local Similarity 96.9%; Pred. No. 5 6e-117;
 Matches 216; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMHACCTVLMHLPAPVAINRKGDPGPGSIQKTYDILVLEHJLHSLAGT 60
 Db 1 mqltagdswgmhaccltvlhlpavainrtcgdpqpgpslqkydltrylehlrlslag 60
 QY 61 YLNLVGPPEFNEPDNPRLGAETLPRATVNLQVWMSLMDRLRLQNTAYSHLDCYLRGL 120
 Db 61 ylnylgppfnepdnpprlgaetlprativdewrslncklrltqneyashllcylrlg1 120
 QY 121 NRQAATLEKRLSLAHFCTSLQGLIGSIAGVWATLGYPLPQPLPCTEPAMAGPAHSDFLQ 180
 Db 121 nrgataeltrslahfctslqglislagymaalgyrlpqlpctepwlpghpsdflq 180
 QY 181 KMDFWLTKELQTLWMSAKDFNRLKKMKQPPAASVTLHEAH 223
 Db 181 kmddfllkeltqlwlrskdfrlkkmqppaaavclhlgah 223

RESULT 11

AAI19587
 ID AAI19587 standard; Protein; 215 AA.

AC AAI19587;

DT 22-JAN-2001 (first entry)

XX Mouse Interleukin-B60 (IL-B60).

XX Interleukin-B60; IL-B60; mouse; cytokine; cytokine-1; factor-1;
 KW haematopoietic; inflammation; anti-inflammatory; autoimmune disease;
 XX therapy.

XX Mus musculus.

XX Key Location/Qualifiers
 FH Peptide 1..17
 FT /label= Signal_peptide
 FT Protein 18..215
 FT /label= Mature-protein

XX W0200053631-A1.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06182.

XX 11-MAR-1999; 99US-0267901.

XX (SCHE) SCHERING CORP.

PI Oppmann B, Timans JC, Kastelein RA, Bazan JF;

DR WPI: 2000-587426/55.
 DR N-PSDB: AAA88547.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
 PT polypeptides, and nucleic acids, useful in research, diagnosis and for
 PT treating inflammatory and autoimmune disorders

XX Claim 1; Page 17; 97pp; English.

XX The present sequence is that of mouse interleukin-B60 (IL-B60), a
 CC novel, small soluble cytokine-like protein that exhibits structural
 CC motifs characteristic of a member of the long-chain cytokines, and
 CC which shows homology to granulocyte colony stimulating factor and
 CC interleukin-6. IL-B60 may have either stimulatory or inhibitory
 CC effects on haematopoietic cells, including e.g. lymphoid cells,
 CC such as T-cells, B-cells, natural killer cells, macrophages,
 CC dendritic cells, haematopoietic progenitors, etc. Methods are
 CC provided for modulating the physiology or development of a cell or
 CC tissue culture cells by contacting the cell with an agonist or
 CC antagonist of IL-B60 or an agonist or antagonist of a complex of
 CC mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see
 CC AAI19588). The IL-B60/CLF-1 cytokine serves as a key physiological

CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.

Sequence 215 AA:

Query Match 95.3%; Score 1167; DB 21; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.6e-115;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 MLaCTVtWHLPAVPALNRTGDPGPGPSIQKTYDTRLYEHQRLSLAGTYVNLGPPFN 70
1 mlaclctvlwlpavpalnrtgdpgpsiqktydtrlyehqrlslagtyvnlgppfn 60
71 EPPFNPRPGAETLPRAVNLVWRSINDRLRLTQNEEAYSHLLCYLGLNRQAATAE LR 130
61 epdlnpprlgaetlpravlntgdpgpsiqktydtrlyehqrlslagtyvnlgppfn 120
131 RSLAHFCTSLQGLGSLGAGVMAATLGYPLPQPLPGTEPAMAPGAHSDPLQKMDFWLLKE 190
121 rslahfctslqglgslgagvmaatlgypplpqlpgtepawapghasdlqkmdfwllke 180
191 LQTWLMSAKDFNRLKKMKOPPAASVTLHLEAHGF 225
181 lqtwlmsakdfnrlkkmkppaasvtlhlea hgf 215

RESULT 12

AAB19586 standard; Protein: 215 AA.

AC AAB19586;

DF 22-JAN-2001 (first entry)

DE Human Interleukin-B60 (IL-B60).

XX Interleukin-B60; IL-B60; human; cytokine; cytokine-like factor-1;
KW haematopoietic; inflammatory; antinflammatory; autoimmune disease;
therapy.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Peptide 1..17 /label= Signal_peptide

XX Protein 18..215 /label= Mature-protein

XX WO200053631-A1.

XX 14-SEP-2000.

XX 09-MAR-2000; 2000WO-US06182.

XX 11-MAR-1999; 99US-0267901.

XX (SCHE) SCHERING CORP.

XX Opmann B, Timans JC, Kastelein RA, Bazan JF;

XX WPI: 2000-587426/55.

XX N-PSDB; AAA88546.

XX Cytokine-like factor 1 (CLF-1) and interleukin (IL)-B60 complexes,
XX polypeptides, and nucleic acids, useful in research, diagnosis and for
XX treating inflammatory and autoimmune disorders

XX Claim 1; Page 15-16; 97pp; English.

XX The present sequence is that of human interleukin-B60 (IL-B60), a
XX novel, small soluble cytokine-like protein that exhibits structural

CC motifs characteristic of a member of the long-chain cytokines, and
CC which shows homology to granulocyte colony stimulating factor and
CC interleukin-6. IL-60B may have either stimulatory or inhibitory
CC effects on haematopoietic cells, including e.g. lymphoid cells,
CC such as T-cells, B-cells, natural killer cells, macrophages,
CC dendritic cells, haematopoietic progenitors, etc. Methods are
CC provided for modulating the physiology or development of a cell or
CC tissue culture cells by contacting the cell with an agonist or
CC antagonist of IL-B60 or an agonist of antagonist of a complex of
CC mature IL-B60 and IL-B60/CLF-1 cytokine serves as a key physiological
CC factor in motor neuron development and regeneration. IL-60B, its
CC agonists and antagonists may be used to treat inflammatory or
CC autoimmune disorders and also for drug screening.

Sequence 215 AA:

Query Match 92.8%; Score 1136; DB 21; Length 215;
Best Local Similarity 96.7%; Pred. No. 3.1e-112;
Matches 208; Conservative 3; Mismatches 4; Indels 1; Gaps 0;

11 MLaCTVtWHLPAVPALNRTGDPGPGPSIQKTYDTRLYEHQRLSLAGTYVNLGPPFN 70
1 mlaclctvlwlpavpalnrtgdpgpsiqktydtrlyehqrlslagtyvnlgppfn 60
71 EPPFNPRPGAETLPRAVNLVWRSINDRLRLTQNEEAYSHLLCYLGLNRQAATAE LR 130
61 epdlnpprlgaetlpravlntgdpgpsiqktydtrlyehqrlslagtyvnlgppfn 120
131 RSLAHFCTSLQGLGSLGAGVMAATLGYPLPQPLPGTEPAMAPGAHSDPLQKMDFWLLKE 190
121 rslahfctslqglgslgagvmaatlgypplpqlpgtepawapghasdlqkmdfwllke 180
191 LQTWLMSAKDFNRLKKMKOPPAASVTLHLEAHGF 225
181 lqtwlmsakdfnrlkkmkppaasvtlhlea hgf 215

RESULT 13

AAM20115 standard; Protein: 164 AA.

AC AAM20115;

DF 12-OCT-2001 (first entry)

XX Peptide #6549 encoded by probe for measuring cervical gene expression.

XX Probe: human; microarray; gene expression; cervical epithelial cell;

XX cervical cancer.

XX Homo sapiens.

XX WO200157278-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US00670.

XX 04-FEB-2000; 2000US-0180312.

XX 26-MAY-2000; 2000US-0207456.

XX 30-JUN-2000; 2000US-0608408.

XX 03-AUG-2000; 2000US-0632366.

XX 21-SEP-2000; 2000US-0234687.

XX 27-SEP-2000; 2000US-0236359.

XX 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SC, Hanzel DK, Chen W, Rank DR;

XX WPI: 2001-488901/53.

XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX

PS Claim 27; SEQ ID No 24941; 487pp; English.

CC The present invention relates to human single exon nucleic acid probes
CC (SENPs: see A110068-A128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human HeLa cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

CC Sequence 164 AA:

Query Match 69.6%; Score 852; DB 22; Length 164;
Best Local Similarity 95.1%; Pred. No. 2.7e-82;
Matches 156; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 62 LNYLGPPEPDPNPRLGAETLPRAVNLVWRSNDRLRLQNYEAYSHLLCYLRLN 121
Db 1 lnylppfnepdnpprlgaktlpratlvdlewrslndkrlrlqnyeyashllcylrlgn 60

OY 122 ROAATAELRSLAHFCTSLGSLGAGMATLGYPLPPLPGEPAWAPGASDFLQK 181
Db 61 rgaataelrslahfctslgslgagmatlgyplpplpgepawapgassdfldqk 120

OY 182 MDPEWLKELQTLWMSAKDFNRLKKMKOPPAASVTLHLEAHGF 225
Db 121 mdfewllkelqtlwmsakdfnrlkkmkoppaasvtlhlgahgf 164

RESULT 14

AAM34012 standard; Protein; 164 AA.

AC AAM34012;

DT 17-OCT-2001 (first entry)

DE Peptide #8049 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001MO-US00663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;

WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX

PS Claim 27; SEQ ID No 34281; 654pp; English.

CC The present invention relates to single exon nucleic acid probes (SENPs:
CC see A1131315-A1157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.

CC Sequence 164 AA:

Query Match 69.6%; Score 852; DB 22; Length 164;
Best Local Similarity 95.1%; Pred. No. 2.7e-82;
Matches 156; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 62 LNYLGPPEPDPNPRLGAETLPRAVNLVWRSNDRLRLQNYEAYSHLLCYLRLN 121
Db 1 lnylppfnepdnpprlgaktlpratlvdlewrslndkrlrlqnyeyashllcylrlgn 60

OY 122 ROAATAELRSLAHFCTSLGSLGAGMATLGYPLPPLPGEPAWAPGASDFLQK 181
Db 61 rgaataelrslahfctslgslgagmatlgyplpplpgepawapgassdfldqk 120

OY 182 MDPEWLKELQTLWMSAKDFNRLKKMKOPPAASVTLHLEAHGF 225
Db 121 mdfewllkelqtlwmsakdfnrlkkmkoppaasvtlhlgahgf 164

RESULT 15

AA09197 standard; Protein; 208 AA.

AC AA09197;

DT 20-JUL-1999 (first entry)

DE Human DNAX interleukin-40 (DIL-40) alternative sequence.

KW DNAX interleukin-40; DIL-40; activation regulation; development;
KW differentiation; hematopoietic; neural cell; drug targeting;

OS Homo sapiens.

PN WO9919491-A2.

PD 22-APR-1999.

PF 13-OCT-1998; 98WO-US20932.

PR 14-OCT-1997; 97US-0950238.

PA (SCHE) SCHERING CORP.

PI Bazan JF, Kastelein RA;

DR WPI; 1999-312475/26.

DR N-PSDB; AAX60797.

PT New human DNAX interleukin-40 (DIL-40) polypeptide and agonists

PS Claim 1; Page 10-11; 76pp; English.

CC The invention relates to a human DNAX interleukin-40 (DIL-40) protein.
CC Host cells containing a vector comprising the DIL-40 nucleic acid can be
CC used for the recombinant expression of the protein. The DIL-40 protein,
CC gene and antibody are useful for regulating activation, development
CC differentiation and function of various cell types, including
CC hematopoietic or neural cells. The antibodies may be anti-DIL-40 agonists, and

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OM protein - protein search, using sw model

Run on: March 18, 2002, 09:31:19 ; Search time 30.45 Seconds
(Without alignments)
166,280 Million cell updates/sec

Title: US-09-931-704-5

Perfect score: 1224
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1224	100.0	225	1	US-08-792-019B-5
2	1224	100.0	225	3	US-08-988-819-5
3	1224	100.0	225	4	US-09-016-534-5
4	1193	97.5	225	1	US-08-792-019B-2
5	1193	97.5	225	3	US-09-106-182-2
6	1193	97.5	225	3	US-08-988-819-2
7	1193	97.5	225	4	US-09-016-534-2
8	118.5	9.7	203	3	US-09-106-182-3
9	110.5	9.0	203	1	US-08-233-609-3
10	110.5	9.0	203	1	US-08-444-083-3
11	110.5	9.0	203	1	US-08-286-304-3
12	110.5	9.0	203	1	US-08-442-745-3
13	110.5	9.0	203	1	US-08-443-129-3
14	110.5	9.0	203	1	US-08-443-952-3
15	110.5	9.0	203	1	US-08-443-130-3
16	110.5	9.0	203	3	US-08-898-911-3
17	110.5	9.0	203	5	PCT-US95-04467-3
18	91.5	7.5	201	1	US-08-444-083-8
19	91.5	7.5	201	1	US-08-286-304-8
20	91.5	7.5	201	1	US-08-442-745-8
21	91.5	7.5	201	1	US-08-443-129-8
22	91.5	7.5	201	1	US-08-443-952-8
23	91.5	7.5	201	1	US-08-443-130-8
24	91.5	7.5	201	1	US-08-792-019B-11
25	91.5	7.5	201	3	US-09-106-182-4
26	91.5	7.5	201	3	US-08-988-819-11
27	91.5	7.5	201	3	US-08-898-911-8

28	91.5	7.5	201	4	US-09-016-534-11	Sequence 11, Appl
29	91.5	7.5	201	5	PCT-US95-04467-8	Sequence 8, Appl
30	90	7.4	195	1	US-07-959-284-5	Sequence 5, Appl
31	90	7.4	195	2	US-08-308-736A-5	Sequence 5, Appl
32	90	7.4	195	5	PCT-US92-08258-2	Sequence 2, Appl
33	90	7.4	195	5	PCT-US93-09649A-5	Sequence 5, Appl
34	90	7.4	195	5	PCT-US93-09649-5	Sequence 5, Appl
35	85.5	7.0	560	2	US-08-756-317-11	Sequence 11, Appl
36	82.5	6.7	2628	4	US-09-413-814-11	Sequence 9, Appl
37	81.5	6.7	582	2	US-08-422-699A-9	Sequence 16, Appl
38	81.5	6.7	582	2	US-08-422-706B-9	Sequence 4, Appl
39	80.5	6.6	379	4	US-09-105-537-16	Sequence 2, Appl
40	80.5	6.6	3782	4	US-09-105-537-4	Sequence 2, Appl
41	79	6.5	1620	1	US-08-542-363-2	Sequence 6, Appl
42	79	6.5	1620	4	US-09-100-089-2	Sequence 6, Appl
43	76.5	6.2	379	4	US-09-320-878-6	Sequence 2, Appl
44	76.5	6.2	388	2	US-08-759-581B-9	Sequence 2, Appl
45	75.5	6.2	593	3	US-08-964-268-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-792-019B-5
; Sequence 5, Application US/08792019B
; Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R. 31,602
REGISTRATION/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-5

Query Match 100.0%; Score 1224; DB 1; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.9e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDLRAGDSWGMCLCTVLMHLPVAPALNRGTGPGPSIOKTYDILKYLH LRSIAGT 60
DB 1 MDLRAGDSWGMCLCTVLMHLPVAPALNRGTGPGPSIOKTYDILKYLH LRSIAGT 60
QY 61 YLYVLPPEPEPFPNPRIGAEFLPRATVNLKWRSLNRLRLTONYFAVS LLYLRL 120
DB 61 YLYVLPPEPEPFPNPRIGAEFLPRATVNLKWRSLNRLRLTONYFAVS LLYLRL 120
QY 121 NROATAEIARRSLAHFCTSIQGLGSIAGVMATLGYPLDPLGTEPMAV AHSDFIQ 180

Db 121 NROAAATLRLSLAHFCTSLQGLGSIAGVATLGYPLPQLPCTEPAMAPGPAHSDFLQ 180
QY 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225
Db 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225

RESULT 2

US-08-988-819-5
; Sequence 5, Application US/08988819
; Patent No. 6054294

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUTROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-988-819-5

Query Match 100.0%; Score 1224; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.9e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTCTVLMHLPVAVPALNRTGDPGSPISQKTYDLTRYLEHQLRSLAGT 60
Db 1 MDLRAGDSWGMCLACTCTVLMHLPVAVPALNRTGDPGSPISQKTYDLTRYLEHQLRSLAGT 60

QY 61 YLNTLGPPNEPDPFNPRIGAEITLPRAIVNLEWMSLNDRLRLTONYEAVSHLLCYLRGL 120
Db 61 YLNTLGPPNEPDPFNPRIGAEITLPRAIVNLEWMSLNDRLRLTONYEAVSHLLCYLRGL 120

QY 121 NROAAATLRLSLAHFCTSLQGLGSIAGVATLGYPLPQLPCTEPAMAPGPAHSDFLQ 180
Db 121 NROAAATLRLSLAHFCTSLQGLGSIAGVATLGYPLPQLPCTEPAMAPGPAHSDFLQ 180

QY 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225
Db 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225

RESULT 3

US-09-016-534-5
; Sequence 5, Application US/09016534
; Patent No. 6143874

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SEMADI, GIORGIO
TITLE OF INVENTION: THE NEUTROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,534
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442B
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-09-016-534-5

Query Match 100.0%; Score 1224; DB 4; Length 225;
Best Local Similarity 100.0%; Pred. No. 5.9e-122;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGMCLACTCTVLMHLPVAVPALNRTGDPGSPISQKTYDLTRYLEHQLRSLAGT 60
Db 1 MDLRAGDSWGMCLACTCTVLMHLPVAVPALNRTGDPGSPISQKTYDLTRYLEHQLRSLAGT 60

QY 61 YLNTLGPPNEPDPFNPRIGAEITLPRAIVNLEWMSLNDRLRLTONYEAVSHLLCYLRGL 120
Db 61 YLNTLGPPNEPDPFNPRIGAEITLPRAIVNLEWMSLNDRLRLTONYEAVSHLLCYLRGL 120

QY 121 NROAAATLRLSLAHFCTSLQGLGSIAGVATLGYPLPQLPCTEPAMAPGPAHSDFLQ 180
Db 121 NROAAATLRLSLAHFCTSLQGLGSIAGVATLGYPLPQLPCTEPAMAPGPAHSDFLQ 180

QY 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225
Db 181 KMDPFWLKLQTLWMSAKDFNRLKKKKMOPPAASVTLHLEAHGF 225

RESULT 4

US-08-792-019B-2
; Sequence 2, Application US/08792019B
; Patent No. 5741772

GENERAL INFORMATION:

APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUTROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA

COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-019B-2

Query Match 97.5% Score 1193; DB 1; Length 225;
Best Local Similarity 96.9% Pred. No. 1.1e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACLTIVLWHLPAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
DB 1 MDLRAGDSWGLACLTIVLWHLPAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
QY 61 YLNYLGPFPNEPDPNPRLGAETLPRAVTVLEWRSINDRLRLTONYEAVSHLLCYRL 120
DB 61 YLNYLGPFPNEPDPNPRLGAETLPRAVTVLEWRSINDRLRLTONYEAVSHLLCYRL 120
QY 121 NROATAELRSLAHFCTSLQGLGSIAGVMAATLGYPLPQPLPGTEPAMAPPAASDFLQ 180
DB 121 NROATAELRSLAHFCTSLQGLGSIAGVMAATLGYPLPQPLPGTEPAMAPPAASDFLQ 180
QY 181 KMDPFWLKELOTWLMRSKADFNRLKKMKOPPAASVTLHLGANGF 225
DB 181 KMDPFWLKELOTWLMRSKADFNRLKKMKOPPAASVTLHLGANGF 225

RESULT 5
US-09-106-182-2
Sequence 2, Application US/09106182
Patent No. 6046035
GENERAL INFORMATION:
APPLICANT: Shi, Yangu
APPLICANT: Ruden, Steve
TITLE OF INVENTION: Cardiotrophin-Like Cytokine
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
STREET: 9410 Key West Ave
CITY: Rockville
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/106,182
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/051,053
FILING DATE: 30-JUN-1997

ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF85
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-106-182-2

Query Match 97.5% Score 1193; DB 3; Length 225;
Best Local Similarity 96.9% Pred. No. 1.1e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MDLRAGDSWGLACLTIVLWHLPAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
DB 1 MDLRAGDSWGLACLTIVLWHLPAVPALNRTGDPGPGSIQKTYDTRYLEHQLRSLAGT 60
QY 61 YLNYLGPFPNEPDPNPRLGAETLPRAVTVLEWRSINDRLRLTONYEAVSHLLCYRL 120
DB 61 YLNYLGPFPNEPDPNPRLGAETLPRAVTVLEWRSINDRLRLTONYEAVSHLLCYRL 120
QY 121 NROATAELRSLAHFCTSLQGLGSIAGVMAATLGYPLPQPLPGTEPAMAPPAASDFLQ 180
DB 121 NROATAELRSLAHFCTSLQGLGSIAGVMAATLGYPLPQPLPGTEPAMAPPAASDFLQ 180
QY 181 KMDPFWLKELOTWLMRSKADFNRLKKMKOPPAASVTLHLGANGF 225
DB 181 KMDPFWLKELOTWLMRSKADFNRLKKMKOPPAASVTLHLGANGF 225

RESULT 6
US-08-988-819-2
Sequence 2, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUTROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-988-819-2

Query Match 97.5%; Score 1193; DB 3; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.1e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 YNTYGPPEPNEPDPNPRIGATLPRATVLEWRSNDRLRLTONYEAVSHLLCYLRGL 120
61 YNTYGPPEPNEPDPNPRIGATLPRATVLEWRSNDRLRLTONYEAVSHLLCYLRGL 120
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
181 KMDDFWLKELQTWLWRSKADFNRLKKMOPPAASVTLHLEAHGF 225
181 KMDDFWLKELQTWLWRSKADFNRLKKMOPPAASVTLHLEAHGF 225

RESULT 7

US-09-016-534-2
Sequence 2, Application US/09016534
Patent No. 6143874

GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI

APPLICANT: ELLIOTT, GARY S.

APPLICANT: SARIENTO, ULLA

APPLICANT: SENALI, GIORGIO

TITLE OF INVENTION: THE NEUTROPHILIC FACTOR NNT-1

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: AMGEN INC.

STREET: ONE AMGEN CENTER

CITY: THOUSAND OAKS

STATE: CA

COUNTRY: USA

ZIP: 91320

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/016,534

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/792,019

FILING DATE: 03-FEB-1997

ATTORNEY/AGENT INFORMATION:

NAME: COOK, ROBERT R.

REGISTRATION NUMBER: 31,602

REFERENCE/DOCKET NUMBER: A-442B

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 225 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-016-534-2

Query Match 97.5%; Score 1193; DB 4; Length 225;
Best Local Similarity 96.9%; Pred. No. 1.1e-118;
Matches 218; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60

1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 MDLRAGDSWGMCLACTCTVLMHLPAYPALNRTGDPGPGSIQKTYDLTRYLEHQLSLAGT 60
1 YNTYGPPEPNEPDPNPRIGATLPRATVLEWRSNDRLRLTONYEAVSHLLCYLRGL 120
61 YNTYGPPEPNEPDPNPRIGATLPRATVLEWRSNDRLRLTONYEAVSHLLCYLRGL 120
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
121 NQQAATAEIRSLAHFCTSLQGLGSIAGVMATLGYPLPQPLPGTEPPMAPGPAHSDFLQ 180
181 KMDDFWLKELQTWLWRSKADFNRLKKMOPPAASVTLHLEAHGF 225
181 KMDDFWLKELQTWLWRSKADFNRLKKMOPPAASVTLHLEAHGF 225

RESULT 8

US-09-106-182-3
Sequence 3, Application US/09106182
Patent No. 6046035

GENERAL INFORMATION:

APPLICANT: Shi, Yanguo

APPLICANT: Ruden, Steve

TITLE OF INVENTION: Cardiotrophin-like Cytokine

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc

STREET: 9410 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/106,182

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/051,053

FILING DATE: 30-JUN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF385

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 203 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-106-182-3

Query Match 97.8%; Score 118.5; DB 3; Length 113;
Best Local Similarity 27.5%; Pred. No. 7.1e-05;
Matches 49; Conservative 26; Mismatches 84; Indels 19; Gaps 6;

40 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 96
40 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 96
40 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 96
27 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 83
27 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 83
27 TQTYDLTRYLEHQLSLAGTYLVNTPPEPNEPDPNPRIL--GAETLLPRATVLEWRS 83
97 LNDRLRLTONYEAVSHLLCYLRGLNQA-----TAELRSLAHFCTSLQGLGSIAGVM 151
97 LNDRLRLTONYEAVSHLLCYLRGLNQA-----TAELRSLAHFCTSLQGLGSIAGVM 151
97 LNDRLRLTONYEAVSHLLCYLRGLNQA-----TAELRSLAHFCTSLQGLGSIAGVM 151
84 -SERLR--QDAALASLPALDAVRRQAEINPRAPRLRLSLLEDAARQVRAI--AAVETVL 140
84 -SERLR--QDAALASLPALDAVRRQAEINPRAPRLRLSLLEDAARQVRAI--AAVETVL 140
84 -SERLR--QDAALASLPALDAVRRQAEINPRAPRLRLSLLEDAARQVRAI--AAVETVL 140

OY 152 ATLCY-----PLPQPLPGTEPAPGAHSDFLQKMDPWLKELQTLWMSAKDFENRL 205
 DB 141 AALGAARGPVPERV-ATSALFTSNSAAGVFSAKVIGLHVCGLYGEMWSRTGDLGOL 197

RESULT 9

US-08-233-609-3
 / Sequence 3, Application US/08233609
 / Patent No. 5534615
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Joffre
 / APPLICANT: Chien, Kenneth
 / APPLICANT: King, Kathleen
 / APPLICANT: Pennica, Diane
 / APPLICANT: Wood, William
 / TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 / NUMBER OF SEQUENCES: 5
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 460 Point San Bruno Blvd
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/233,609
 / FILING DATE: 25-APR-1994
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER:
 / FILING DATE:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Hasak, Janet E.
 / REGISTRATION NUMBER: 28,616
 / REFERENCE/DOCKET NUMBER: 894
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/952-1896
 / TELEFAX: 415/952-9881
 / TELEX: 910/371-7168
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 203 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / US-08-233-609-3

Query Match 9.0%; Score 110.5; DB 1; Length 203;
 Best Local Similarity 27.4%; Pred. No. 0.0005;
 Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

OY 40 IOKTYDITRYLEHQRSLAGTYLNTGPPNEBDFNPPRL---GAETLRATYNLEWMS 96
 DB 27 IROTHNLARLTLYEAQLEBYVOOGEPGLPGFSPRLPLAGLSGPAVSHAGLPV--- 83
 OY 97 LNDRLRLQNYEAYSHLLCYLRGLNROA-----TALRSLAHFCSLQGLGSIAGVM 151
 DB 84 -SERLR--QDAALSVLPALDLAVRRQALNRPAPRLSLSDAARQVRAVETVL 140
 OY 152 ATLCYPLPQPLPGTEPA-----WAPGAHSDFLQKMDPWLKELQTLWMSAKDFENRL 205
 DB 141 AALGAARGPVPERV-ATSALFTSNSAAGVFSAKVIGLHVCGLYGEMWSRTGDLGOL 197

RESULT 10
 US-08-444-083-3
 / Sequence 3, Application US/08444083
 / Patent No. 5571675

GENERAL INFORMATION:
 / APPLICANT: Baker, Joffre
 / APPLICANT: Chien, Kenneth
 / APPLICANT: King, Kathleen
 / APPLICANT: Pennica, Diane
 / APPLICANT: Wood, William
 / TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 460 Point San Bruno Blvd
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/444,083
 / FILING DATE: 17-MAY-1995
 / CLASSIFICATION: 435
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/233609
 / FILING DATE: 25-APR-1994
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/286304
 / FILING DATE: 05-AUG-1994
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Torchia, Timothy E.
 / REGISTRATION NUMBER: 36,700
 / REFERENCE/DOCKET NUMBER: 894P1D5
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 415/925-8674
 / TELEFAX: 415/952-9881
 / TELEX: 910/371-7168
 / INFORMATION FOR SEQ ID NO: 3:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 203 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / US-08-444-083-3

Query Match 9.0%; Score 110.5; DB 1; Length 203;
 Best Local Similarity 27.4%; Pred. No. 0.0005;
 Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

OY 40 IOKTYDITRYLEHQRSLAGTYLNTGPPNEBDFNPPRL---GAETLRATYNLEWMS 96
 DB 27 IROTHNLARLTLYEAQLEBYVOOGEPGLPGFSPRLPLAGLSGPAVSHAGLPV--- 83
 OY 97 LNDRLRLQNYEAYSHLLCYLRGLNROA-----TALRSLAHFCSLQGLGSIAGVM 151
 DB 84 -SERLR--QDAALSVLPALDLAVRRQALNRPAPRLSLSDAARQVRAVETVL 140
 OY 152 ATLCYPLPQPLPGTEPA-----WAPGAHSDFLQKMDPWLKELQTLWMSAKDFENRL 205
 DB 141 AALGAARGPVPERV-ATSALFTSNSAAGVFSAKVIGLHVCGLYGEMWSRTGDLGOL 197

RESULT 11
 US-08-286-304-3
 / Sequence 3, Application US/08286304
 / Patent No. 5571893
 / GENERAL INFORMATION:
 / APPLICANT: Baker, Joffre
 / APPLICANT: Chien, Kenneth
 / APPLICANT: King, Kathleen
 / APPLICANT: Pennica, Diane
 / APPLICANT: Wood, William

TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,304
FILING DATE: 05-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 894P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-286-304-3

Query Match
Best Local Similarity 27.4%; Score 110.5; DB 1; Length 203;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IOKTYDLTRYLEHQLSLAGTYLNTGPPNEPDPNPRL---GAETLPRAVNLFWRS 96
DB 27 IROHNLARLLTKYAEOLEEVYQOGEPFGIPSPRLPLAGISGPASHAGLPV--- 83
QY 97 LNDRLRLTONTYEAASHLLCYLRGLNRQA-----TAELRSLAHFCTSLQGLLSIAGYM 151
DB 84 -SERLR--QDAALSVLPALLDAVRRROAELNRPAPRLRLSLSDAAROVRAALCAVEYVL 140
QY 152 ATLGYPPLPQPLGTEPA-----WAPGPAHSDFLOKMDDFWLKELQTLWLRSAKDPENRL 205
DB 141 AALGAARG--PGPEPVYATLTFTANSTAGISAKVLGFHVGLGVEWVSRTFGDLGOL 197

RESULT 12
US-08-442-745-3
Sequence 3, Application US/08442745
Patent No. 5624806
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 894P1D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 203 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-442-745-3

Query Match
Best Local Similarity 27.4%; Score 110.5; DB 1; Length 203;
Matches 49; Conservative 23; Mismatches 86; Indels 21; Gaps 6;

QY 40 IOKTYDLTRYLEHQLSLAGTYLNTGPPNEPDPNPRL---GAETLPRAVNLFWRS 96
DB 27 IROHNLARLLTKYAEOLEEVYQOGEPFGIPSPRLPLAGISGPASHAGLPV--- 83
QY 97 LNDRLRLTONTYEAASHLLCYLRGLNRQA-----TAELRSLAHFCTSLQGLLSIAGYM 151
DB 84 -SERLR--QDAALSVLPALLDAVRRROAELNRPAPRLRLSLSDAAROVRAALCAVEYVL 140
QY 152 ATLGYPPLPQPLGTEPA-----WAPGPAHSDFLOKMDDFWLKELQTLWLRSAKDPENRL 205
DB 141 AALGAARG--PGPEPVYATLTFTANSTAGISAKVLGFHVGLGVEWVSRTFGDLGOL 197

RESULT 13
US-08-443-129-3
Sequence 3, Application US/08443129
Patent No. 5627073
GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:

